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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2004, 03:36:17 ; Search time 361 Seconds

(without alignments)
3098.044 Million cell updates/sec

Title: US-10-063-732-120

Perfect score: 1172

Sequence: 1 MATHALEIAGLPLGVGMVG.....QKSYHTKKSPVRSQIV 225

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	1172	100.0	1793	9	US-09-731-872-164	Sequence 164, App
	3	1172	100.0	1793	10	US-09-876-997-164	Sequence 164, App
	4	1172	100.0	2010	10	US-09-946-374-327	Sequence 327, App
	5	1172	100.0	2010	12	US-10-015-395A-327	Sequence 327, App
	6	1172	100.0	2010	13	US-10-206-915-357	Sequence 357, App
	7	1172	100.0	2010	13	US-10-199-670-357	Sequence 357, App
	8	1172	100.0	2010	13	US-10-201-858-357	Sequence 357, App
	9	1172	100.0	2010	13	US-10-205-890-357	Sequence 357, App
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	11	1172	100.0	2010	13	US-10-201-853-357	Sequence 357, App
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	19	1172	100.0	2010	13	US-10-176-483-357	Sequence 357, App
	20	1172	100.0	2010	13	US-10-176-749-357	Sequence 357, App
	21	1172	100.0	2010	13	US-10-176-914-357	Sequence 357, App
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	23	1172	100.0	2010	13	US-10-006-485A-327	Sequence 327, App
	24	1172	100.0	2010	13	US-10-013-907A-327	Sequence 327, App
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	28	1172	100.0	2010	13	US-10-063-594-119	Sequence 119, App
	29	1172	100.0	2010	13	US-10-063-553-119	Sequence 119, App
	30	1172	100.0	2010	13	US-10-063-554-119	Sequence 119, App
	31	1172	100.0	2010	13	US-10-176-484-357	Sequence 357, App
	32	1172	100.0	2010	13	US-10-180-550-357	Sequence 357, App
	33	1172	100.0	2010	13	US-10-183-014-357	Sequence 357, App
	34	1172	100.0	2010	13	US-10-187-738-357	Sequence 357, App
	35	1172	100.0	2010	13	US-10-187-740-357	Sequence 357, App
	36	1172	100.0	2010	13	US-10-187-883-357	Sequence 357, App
	37	1172	100.0	2010	13	US-10-194-363-357	Sequence 357, App
	38	1172	100.0	2010	13	US-10-194-460-357	Sequence 357, App
	39	1172	100.0	2010	13	US-10-194-463-357	Sequence 357, App
	40	1172	100.0	2010	13	US-10-194-484-357	Sequence 357, App
	41	1172	100.0	2010	13	US-10-195-884-357	Sequence 357, App
	42	1172	100.0	2010	13	US-10-195-896-357	Sequence 357, App
	43	1172	100.0	2010	13	US-10-196-744-357	Sequence 357, App
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	45	1172	100.0	2010	13	US-10-196-757-357	Sequence 357, App

ALIGNMENTS

RESULT 1

US-10-029-386-22722/c

; Sequence 22722, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AEMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 22722

; LENGTH: 678

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AP000884.1

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.97

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
 OTHER INFORMATION: SWISSPROT HIT: P56748, EVALUE 1.00e-120
 OTHER INFORMATION: NT HIT: G114780163, EVALUE 0.00e+00
 OTHER INFORMATION: EST_HUMAN HIT: AUL21779.1, EVALUE 0.00e+00
 US-10-029-386-22722

Alignment Scores:
 Pred. No.: 2,76e-150 Length: 678
 Score: 1172.00 Matches: 225
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-063-732-120 (1-225) x US-10-029-386-22722 (1-678)

QY	1	MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly	20
DB	678	ATGGCAACCCATGCCCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGAATGGTGGC	619
QY	21	ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheLeuGluAsnIle	40
DB	618	ACAGTGGCTGCTACTGTCATGCCCTCAGTGGAGAGTGTGGCTTCATTTGAAACCAATC	559
QY	41	ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle	60
DB	558	GTGGTTTTTGAACACTTCTGGAGAGACTGTGATGATTCGCTGGCTCTTTCTCGGACCTACAGCGAGC	499
QY	61	ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla	80
DB	498	AGGATGCAGTGCACCAATCTATGATTCCTGCTGGCTCTTTCTCGGACCTACAGCGAGC	439
QY	81	ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	100
DB	438	AGAGGACTGATGTGTGCTGCTTCCTGCTGATGCTTCTTGGCTTTTCATGATGGCCATCCTT	379
QY	101	GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValIysAlaHisIleLeuLeu	120
DB	378	GGCAGTAAATGCACAGGTGCACGGGGACATGAGAGGTGAAGGCTCACATTTCTGCTG	319
QY	121	ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal	140
DB	318	ACGCTGGAAATCATCTTCATCATCACGGGCATGCTGCTCATCTCCCTGTGAGCTGGGT	259
QY	141	AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu	160
DB	258	GCCAAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTGCCCAAAACGTGAG	199
QY	161	LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla	180
DB	198	CTTGAGAGACTCTCTACTTAGGATGGACCGGACCTGGTGTGCTGATTTGGAGAGCT	139
QY	181	LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro	200
DB	138	CTGTCTGCTCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTTCGATACCT	79
QY	201	SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer	220
DB	78	TCCCATCGCACAAACCAAAAGTTATCACCGGAAAGAGTCAACCGAGGCTCTACTCC	19
QY	221	ArgSerGlnTyrVal	225
DB	18	AGAAGTCAATGTGTG	4

RESULT 2

US-09-731-872-164
 Sequence 164, Application US/09731872
 Patent No. US20020102604A1
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Bouqueleret, Lydie
 APPLICANT: Jobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
 FILE REFERENCE: 78.053.REG
 CURRENT APPLICATION NUMBER: US/09/731,872
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,629
 PRIOR FILING DATE: 1999-12-08
 PRIOR APPLICATION NUMBER: US 60/187,470
 PRIOR FILING DATE: 2000-03-06
 NUMBER OF SEQ ID NOS: 482
 SOFTWARE: Patent.pm
 SEQ ID NO 164
 LENGTH: 1793
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 173..847
 US-09-731-872-164

Alignment Scores:
 Pred. No.: 1,29e-149 Length: 1793
 Score: 1172.00 Matches: 225
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-063-732-120 (1-225) x US-09-731-872-164 (1-1793)

QY	1	MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly	20
DB	173	ATGGCAACCCATGCCCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGAATGGTGGC	232
QY	21	ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheLeuGluAsnIle	40
DB	233	ACAGTGGCTGCTACTGTCATGCCCTCAGTGGAGAGTGTGGCTTCATTTGAAACCAATC	292
QY	41	ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle	60
DB	293	GTGGTTTTTGAACACTTCTGGAGAGACTGTGATGATTCGCTGGCTTTTCATGATGGCCATCCTT	352
QY	61	ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla	80
DB	353	AGGATGCAGTGCACCAATCTATGATTCCTGCTGGCTCTTTCTCGGACCTACAGCGAGC	412
QY	81	ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	100
DB	413	AGAGGACTGATGTGTGCTGCTTCCTGCTGATGCTTCTTGGCTTTTCATGATGGCCATCCTT	472
QY	101	GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValIysAlaHisIleLeuLeu	120
DB	473	GGCAGTAAATGCACAGGTGCACGGGGACAAATGAGAGGTGAAGGCTCACATTTCTGCTG	532
QY	121	ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal	140
DB	533	ACGCTGGAAATCATCTTCATCATCACGGGCATGCTGCTCATCTCCCTGTGAGCTGGGT	592
QY	141	AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu	160
DB	593	GCCAAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTGCCCAAAACGTGAG	652
QY	161	LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla	180
DB	653	CTTGAGAGACTCTCTACTTAGGATGGACCGGACCTGGTGTGCTGATTTGGAGAGCT	712
QY	181	LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro	200
DB	713	CTGTCTGCTCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACTTCGATACCT	772
QY	201	SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer	220
DB	773	TCCCATCGCACAAACCAAAAGTTATCACCGGAAAGAGTCAACCGAGGCTCTACTCC	832

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QY 221 ArgSerGlnTyrVal 225
Db 833 AGAAGTCAGTATGTG 847

RESULT 3
US-09-876-997-164
; Sequence 164, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouquellet, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.054.CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 164
; LENGTH: 1793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 173..847
US-09-876-997-164

Alignment Scores:
Pred. No.: 1,29e-149 Length: 1793
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-063-732-120 (1-225) x US-09-876-997-164 (1-1793)

QY 1 MetAlaThrHisAlaLeuGluHisAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 173 ATGGCAACCCAGCTTAGAATCGCTGGCTGTTCTTGGTGGTGGTGGTGGTGGTGGC 232
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle 40
Db 233 ACAGTGGCTGTCACTGTCAATGCCCTCAGTGGAGAGTGTGGCTTTCAATGAAACCAACATC 292
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
Db 293 GTGGCTTTTGAACACTCTGGAGAGGACTGTGGATGAATTCGTGGAGCAGGCTTACATC 352
QY 61 ArgMetGlnCysLysIleTyrAspSerIleuAlaLeuSerProAspLeuGlnAlaAla 80
Db 353 AGGATGCAGTCAAAATCTATGATTCCTGCTGCTCTTTCTCCGGACCTACAGGCAGCC 412
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheIleuAlaPheMetMetAlaIleLeu 100
Db 413 AGAGGACTGATGTGTGCTGTCTTCGTGATGTCCTTCTTGGCTTTTCATGATGCCATCCTT 472
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 473 GGCATGAATGCACAGGTGCACGGGGACAAATGAGAGGTGAAGGCTTCACTTCGCTG 532
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 533 ACGGCTGGAATCATCTTCATCATCACGGGCATGTGGTGTCTCATCCCTGTGAGCTGGTT 592
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
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Db 593 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAAAACGTTGAG 652
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180
Db 653 CTGGAGAGAGCTCTCTACTTATAGATGGACCCAGGACCTGGTCTGATTGTTGGAGAGCT 712
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
Db 713 CTGTTCTGCTGCTGTTTTTTGTTGCAACGAAAGACAGCTAGCTACAGATACCTCGATACCT 772
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 773 TCCATCCCAACCAACCAAAAGTTATCACACCGGAAAGAGTCAACCGAGCGCTCTACTCC 832
QY 221 ArgSerGlnTyrVal 225
Db 833 AGAAGTCAGTATGTG 847

RESULT 4
US-09-946-374-327
; Sequence 327, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
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us-10-063-732-120.rnpb

Fri Sep 3 10:15:58 2004

1 PRIOR APPLICATION NUMBER: 60/099741
2 PRIOR FILING DATE: 1998-09-10
3 PRIOR APPLICATION NUMBER: 60/099754
4 PRIOR FILING DATE: 1998-09-10
5 PRIOR APPLICATION NUMBER: 60/099763
6 PRIOR FILING DATE: 1998-09-10
7 PRIOR APPLICATION NUMBER: 60/099792
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9 PRIOR APPLICATION NUMBER: 60/099808
10 PRIOR FILING DATE: 1998-09-10
11 PRIOR APPLICATION NUMBER: 60/099812
12 PRIOR FILING DATE: 1998-09-10
13 PRIOR APPLICATION NUMBER: 60/099815
14 PRIOR FILING DATE: 1998-09-10
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17 PRIOR APPLICATION NUMBER: 60/100385
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19 PRIOR APPLICATION NUMBER: 60/100388
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21 PRIOR APPLICATION NUMBER: 60/100390
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23 PRIOR APPLICATION NUMBER: 60/100584
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27 PRIOR APPLICATION NUMBER: 60/100661
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48 PRIOR FILING DATE: 1998-09-17
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51 PRIOR APPLICATION NUMBER: 60/101068
52 PRIOR FILING DATE: 1998-09-18
53 PRIOR APPLICATION NUMBER: 60/101071
54 PRIOR FILING DATE: 1998-09-18
55 PRIOR APPLICATION NUMBER: 60/101279
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57 PRIOR APPLICATION NUMBER: 60/101471
58 PRIOR FILING DATE: 1998-09-23
59 PRIOR APPLICATION NUMBER: 60/101472
60 PRIOR FILING DATE: 1998-09-23
61 PRIOR APPLICATION NUMBER: 60/101474
62 PRIOR FILING DATE: 1998-09-23
63 PRIOR APPLICATION NUMBER: 60/101475
64 PRIOR FILING DATE: 1998-09-23
65 PRIOR APPLICATION NUMBER: 60/101476
66 PRIOR FILING DATE: 1998-09-23
67 PRIOR APPLICATION NUMBER: 60/101477
68 PRIOR FILING DATE: 1998-09-23
69 PRIOR APPLICATION NUMBER: 60/101479
70 PRIOR FILING DATE: 1998-09-23
71 PRIOR APPLICATION NUMBER: 60/101738
72 PRIOR FILING DATE: 1998-09-24
73 PRIOR APPLICATION NUMBER: 60/101741

74 PRIOR FILING DATE: 1998-09-24
75 PRIOR APPLICATION NUMBER: 60/101743
76 PRIOR FILING DATE: 1998-09-24
77 PRIOR APPLICATION NUMBER: 60/101915
78 PRIOR FILING DATE: 1998-09-24
79 PRIOR APPLICATION NUMBER: 60/101916
80 PRIOR FILING DATE: 1998-09-24
81 PRIOR APPLICATION NUMBER: 60/102207
82 PRIOR FILING DATE: 1998-09-29
83 PRIOR APPLICATION NUMBER: 60/102240
84 PRIOR FILING DATE: 1998-09-29
85 PRIOR APPLICATION NUMBER: 60/102307
86 PRIOR FILING DATE: 1998-09-29
87 PRIOR APPLICATION NUMBER: 60/102330
88 PRIOR FILING DATE: 1998-09-29
89 PRIOR APPLICATION NUMBER: 60/102331
90 PRIOR FILING DATE: 1998-09-29
91 PRIOR APPLICATION NUMBER: 60/102484
92 PRIOR FILING DATE: 1998-09-30
93 PRIOR APPLICATION NUMBER: 60/102487
94 PRIOR FILING DATE: 1998-09-30
95 PRIOR APPLICATION NUMBER: 60/102570
96 PRIOR FILING DATE: 1998-09-30
97 PRIOR APPLICATION NUMBER: 60/102571
98 PRIOR FILING DATE: 1998-09-30
99 PRIOR APPLICATION NUMBER: 60/102684
100 PRIOR FILING DATE: 1998-10-01
101 PRIOR APPLICATION NUMBER: 60/102687
102 PRIOR FILING DATE: 1998-10-01
103 PRIOR APPLICATION NUMBER: 60/102965
104 PRIOR FILING DATE: 1998-10-02
105 PRIOR APPLICATION NUMBER: 60/103258
106 PRIOR FILING DATE: 1998-10-06
107 PRIOR APPLICATION NUMBER: 60/103314
108 PRIOR FILING DATE: 1998-10-07
109 PRIOR APPLICATION NUMBER: 60/103315
110 PRIOR FILING DATE: 1998-10-07
111 PRIOR APPLICATION NUMBER: 60/103328
112 PRIOR FILING DATE: 1998-10-07
113 PRIOR APPLICATION NUMBER: 60/103395
114 PRIOR FILING DATE: 1998-10-07
115 PRIOR APPLICATION NUMBER: 60/103396
116 PRIOR FILING DATE: 1998-10-07
117 PRIOR APPLICATION NUMBER: 60/103401
118 PRIOR FILING DATE: 1998-10-07
119 PRIOR APPLICATION NUMBER: 60/103449
120 PRIOR FILING DATE: 1998-10-06
121 PRIOR APPLICATION NUMBER: 60/103633
122 PRIOR FILING DATE: 1998-10-08
123 PRIOR APPLICATION NUMBER: 60/103678
124 PRIOR FILING DATE: 1998-10-08
125 PRIOR APPLICATION NUMBER: 60/103679
126 PRIOR FILING DATE: 1998-10-08
127 PRIOR APPLICATION NUMBER: 60/103711
128 PRIOR FILING DATE: 1998-10-08
129 PRIOR APPLICATION NUMBER: 60/104257
130 PRIOR FILING DATE: 1998-10-14
131 PRIOR APPLICATION NUMBER: 60/104987
132 PRIOR FILING DATE: 1998-10-20
133 PRIOR APPLICATION NUMBER: 60/105000
134 PRIOR FILING DATE: 1998-10-20
135 PRIOR APPLICATION NUMBER: 60/105002
136 PRIOR FILING DATE: 1998-10-20
137 PRIOR APPLICATION NUMBER: 60/105104
138 PRIOR FILING DATE: 1998-10-21
139 PRIOR APPLICATION NUMBER: 60/105169
140 PRIOR FILING DATE: 1998-10-22
141 PRIOR APPLICATION NUMBER: 60/105266
142 PRIOR FILING DATE: 1998-10-22
143 PRIOR APPLICATION NUMBER: 60/105693
144 PRIOR FILING DATE: 1998-10-26
145 PRIOR APPLICATION NUMBER: 60/105694
146 PRIOR FILING DATE: 1998-10-26

; PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:

Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-063-732-120 (1-225) x US-09-946-374-327 (1-2010)

```
QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
DB 97 ATGGCAACCCAGCTTAGAAATCGCTGGCTGTTCTTGGTGGTGGTGGTGGTGGTGGC 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
DB 157 ACAGTGGCTGTACCTCATGCTCAGTGGAGAGTGTGGCCCTTATTGAAACCAACATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
DB 217 GTGGTTTTTGAAACTTCTGGAGAGACTGTGCATGCAATTGGCTGAGGCGAGCTTAACATC 276
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerProAspLeuGlnAlaAla 80
DB 277 AGGATGCAGTGCAGAAATCTATGATTCCTGCTGGCTCTTCTCCGAGCCTACAGGCAGCC 336
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
DB 337 AGAGGACTGATGTGCTGCTTCCTGATGTCCTTCTTGGCTTTTATGATGCCATCCTT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
DB 397 GGCATGAAATGCACAGGTGCACGGGGACAATGAGAGGTGAGGCTCACATTCCTGCTG 456
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
DB 457 ACGGTGGAATCATCTTTCATCATCCGGGCATGGTGGTGTCTATCCCTGTGAGCTGGCTT 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
DB 517 GCCATGCAATCATCAGAGATTTCTATACTCAATAGTGAATGTGCCCAAAACGTGAG 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
DB 577 GTGGAGAGACTCTCTACTTAGGATGACACAGGCACTGGTGTCTGTTGAGGAGACT 636
QY 181 LeuPheCysValPheCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
DB 637 CTGTTCTGCTCGTGTGTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACCTCGATACCT 696
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
DB 697 TCCCATCGCAACCCCAAAAGTTATCACCCGGAAGAGTACCCGAGGCTCTACTCC 756
QY 221 ArgSerGlnTyrVal 225
DB 757 AGAAGTCAGTAGTG 771
```

RESULT 5

; Sequence 327, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 327
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-015-395A-327

Alignment Scores:

Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-063-732-120 (1-225) x US-10-015-395A-327 (1-2010)

```
QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
DB 97 ATGGCAACCCAGCTTAGAAATCGCTGGCTGTTCTTGGTGGTGGTGGTGGTGGTGGC 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
DB 157 ACAGTGGCTGTACCTCATGCTCAGTGGAGAGTGTGGCTTTCATTTGAAACCAACATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
DB 217 GTGGTTTTTGAAACTTCTGGAGAGACTGTGGATGAAATTCGGTGGAGCAGCTTAACATC 276
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
DB 277 AGGATGCAGTGCAGAAATCTATGATTCCTGCTGGCTCTTCTCCGAGCCTACAGGCAGCC 336
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
DB 337 AGAGGACTGATGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTTCATGATGCCATCCTT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
DB 397 GGCATGAAATGCACAGGTGCACGGGGACAATGAGAGGTGAGGCTCACATTCCTGCTG 456
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
DB 457 ACGGTGGAATCATCTTTCATCATCCGGGCATGGTGGTGTCTATCCCTGTGAGCTGGCTT 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
DB 517 GCCAATGCCATCATCAGAGATTTCTATACTCAATAGTGAATGTGCCCAAAACGTGAG 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
DB 577 GTGGAGAGACTCTCTACTTAGGATGACACAGGCACTGGTGTCTGTTGAGGAGACT 636
QY 181 LeuPheCysValPheCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
DB 637 CTGTTCTGCTGGTGTGTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACCTCGATACCT 696
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
DB 697 TCCCATCGCAACCCCAAAAGTTATCACCCGGAAGAGTATCACCCGGAAGAGTACCCGAGGCTCTACTCC 756
```

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QY 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 6
US-10-206-915-357
; Sequence 357, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-206-915-357

Alignment Scores:
Pred. No.: 1,54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-206-915-357 (1-2010)
QY 1 MetAlaThrHisAlaLeuGluIleAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGGCAACCCCAAGCTTAGAATCGCTGGCTGTTCTTGGTGTGTGGTATGGTGGGC 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle 40
Db 157 ACATGGCTGTGACATGTGTCATGCCCTCAGTGAGAGTGGCTTCATTGAAACCAACATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60

217 GTGGTTTTTGAACCTTCTGGGAAGAGCTGTGGATGAATTGGTGGAGGAGGCTAACATC 276
61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaLa 80
277 AGGATGCAGTGCAGAAATCTATGATTCCTGGCTCTTTCTCCGACCTACAGGAGGCC 336
81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
337 AGAGGACTGATGTGTCTCTCCGTGATGCTCTTCTGGCTTTTCATGTATGGCCATCCCT 396
101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
397 GGCATGAAATGCACAGGTGCAGGGGACAAATGAGAAAGGTGAGAGCTCACATTCGTG 456
121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
457 ACGGCTGGAATCATCTTCATCATCGGCGCATGGTGGTGTCTCATCCCTGTGAGCTGG 516
141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
517 GCCAATGCCATCATCAGAGATTCTATACTCAATAGTGAATGTTGCCCAAAACGTGAG 576
161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
577 CTTGGAGAGCTCTCTACTTAGATGACACACGGCACTGGTGTGATTGTTGGAGAGCT 636
181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
637 CTGTTCTGCTGCGTTTTTTTGTGCAACGAAAGAGCAGTAGCTACAGATACCTGATAC 696
201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
697 TCCCATCGCACAAACCCCAAAAGTTATCACCCGGAAGAAGTACACCGGCGTCTACTCC 756
221 ArgSerGlnTyrVal 225
757 AGAAGTCAGTATGTG 771

RESULT 7
US-10-199-670-357
; Sequence 357, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
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/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 357
/ LENGTH: 2010
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-199-670-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-199-670-357 (1-2010)
QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly 20
DB 97 ATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGGATGTGGGC 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheLeuGluAsnIle 40
DB 157 ACAGTGGCTGTCACTGTCAATGCCTCAGTGGAGAGTGTGGCCTTCATTGAAACACATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
DB 217 GTGCTTTTGAATACTCTGGGAAGACTGTGGAGAGTGTGGAGGCTTAACATC 276
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAla 80
DB 277 AGGATGCGATGATGCTGCTCCGTGATGTCCTTCTTGGCTTTTATGATGCCATCCT 396
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
DB 337 AGAGGACTGATGCTGCTCCGTGATGTCCTTCTTGGCTTTTATGATGCCATCCT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
DB 397 GGCAATGAATGCACAGGTGCACGGGGACCAATGAGAAGTGAAGGCTCACATTCGCTG 456
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
DB 457 ACGCTGGATCATCTTCATCATCAGGGGACATGGTGGTGGTCCCTCGTGGCTGGGT 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
DB 517 GCCAATGCCATCATCAGAGATTTCTATAACTCATAGTGAATGTGCCCAAAACGGTGA 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyVala 180
DB 577 CTGGAGAAGCTCTCTACTTAGGATGACCAACGACCTGGTGGTGGTGGTGGTGGTGGT 636
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 200
DB 637 CTGTTCTGCTGCGTTTTTGTGTGCAACGAAAGACAGTGTAGTACAGATCTCGATACCT 696
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
DB 697 TCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAGTACCAGAGGCTCTACTCC 756
QY 221 ArgSerGlnTyrVal 225
DB 757 AGAAGTCAGTATGTG 771

RESULT 8
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; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 357
 ; LENGTH: 2010
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-205-890-357

Alignment Scores:
 Pred. No.: 1-54e-149 Length: 2010
 Score: 1172.00 Matches: 225
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-205-890-357 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyValGlyMetValGly 20
 Db 97 ATGGCAACCCATGCGCTTAGAAATCGCTGGGCTGTTCTTGGTGGTGTGAATGGTGGC 156
 QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheLeuGluAsnAsnile 40
 Db 157 ACAGTGGCTGCTACTGTCATGCCCTCAGTGGAGAGTGTGGCCTTCATTGAAACAAACATC 216
 QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnile 60
 Db 217 GTGGTTTTGAAACATCTGGGAAGGACTGTGGATGAATTCGTGGAGGAGGTAAATC 276
 QY 61 ArgMetGlnCysLysLysLeuTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80
 Db 277 AGGATGCAAGTCAAAATCTATGATTCCTGCTGCTCTTCTCCGGACCTACAGGAGGCC 336
 QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaLeu 100
 Db 337 AGAGGAGTGAATGCTGCTGCTTCCGTGATGTCCTTCTTGGCTTCATGATGGCCATCCTT 396
 QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisLeuLeu 120
 Db 397 GGCATGAATGACACAGTGCACGGGGGCAATGAGAAGGTGAAGGCTCACATTCTGCTG 456
 QY 121 ThrAlaGlyLeuLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
 Db 457 ACGGCTGGAATCATCTTCATCATCATCAGGGCATGCTGGTGTCTCCTCTGAGCTGGGTT 516
 QY 141 AlaAsnAlaLeuLeuArgAspPheTyrAsnSerLeuValAsnValAlaGlnLysArgGlu 160
 Db 517 GCCAATGCCATCATCAGAGATTTCTATACTCAATAGTAGATGTTGCCCAAAAGGTGAG 576
 QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuLeuValGlyGlyAla 180
 Db 577 CTTCGAGAGAGCTCTCTACTTAGGATGACACCGCATGCTGGTGTCTGATTGTTGGAGGAGCT 636
 QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerSerSerTyrArgTyrSerLeuPro 200
 Db 637 CTGTTCTGCTGCTGTTTTTGTTCACAAAGAGAGCAGTAGCTACAGATATCTGATACCT 696
 QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
 Db 697 TCCCATCGCACAAACCCAAAAAGTTATCACCCGGAAAGAGTACACCGAGGCTCTACTCC 756
 QY 221 ArgSerGlnTyrVal 225
 Db 757 AGAAGTCAGTATGTG 771

RESULT 10
 US-10-208-024-357
 ; Sequence 357, Application US/10208024
 ; Publication No. US20040048335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.

QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaLeu 100
 Db 337 AGAGGAGTGAATGCTGCTTCCGGAGATGCTCTTGGCTTCTATGATGGCCATCCTT 396
 QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisLeuLeu 120
 Db 397 GGCATGAATGACACAGTGCACGGGGGCAATGAGAAGGTGAAGGCTCACATTCTGCTG 456
 QY 121 ThrAlaGlyLeuLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
 Db 457 ACGGCTGGAATCATCTTCATCATCAGGGCATGCTGGTGTCTCATCCCTGTGAGCTGGGT 516
 QY 141 AlaAsnAlaLeuLeuArgAspPheTyrAsnSerLeuValAsnValAlaGlnLysArgGlu 160
 Db 517 GCCAATGCCATCATCAGAGATTTCTATACTCAATAGTAGATGTTGCCCAAAAGGTGAG 576
 QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuLeuValGlyGlyAla 180
 Db 577 CTTCGAGAGAGCTCTCTACTTAGGATGACACCGCATGCTGGTGTCTGATTGTTGGAGGAGCT 636
 QY 181 LeuPheCysCysValPheCysAsnGluLysSerSerSerTyrArgTyrSerLeuPro 200
 Db 637 CTGTTCTGCTGCTGTTTTTGTTCACAAAGAGAGCAGTAGCTACAGATATCTGATACCT 696
 QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
 Db 697 TCCCATCGCACAAACCCAAAAAGTTATCACCCGGAAAGAGTACACCGAGGCTCTACTCC 756
 QY 221 ArgSerGlnTyrVal 225
 Db 757 AGAAGTCAGTATGTG 771

RESULT 9
 US-10-205-890-357
 ; Sequence 357, Application US/10205890
 ; Publication No. US20040048334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C519
 ; CURRENT FILING DATE: 2002-07-26
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28


```

; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-357

Alignment Scores:
Pred. No.: 1.54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-208-024-357 (1-2010)

Qy 1 MetAlaThrHisAlaLeuGluAlaGlyLeuPheLeuGlyValGlyMetValGly 20
Db 97 ATGCCAACCCAGCTTAGAATCGCTGGGTGTTCTGTGGTGTGGTGGTGGC 156

Qy 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheLeuAsnAsnile 40
Db 157 ACATGGCTGTCACTGTCATGCTCAGTGGAGGTGCTGGCTTCATTGAAACACATC 216

Qy 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnile 60
Db 217 GTGGTTTTTGAAGAACTTCGGGAAGGACTGTGGATGAATTCGTCGAGCGCTAACATC 276

Qy 61 ArgMetGlnCysLysLleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAala 80
Db 277 AGGAGCTGAGTCAAAATCTATGATTCCTCGCTCTTTCTCCGGAGCTACAGGCAGCC 336

Qy 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
Db 337 AGAGGACTGATGTGCTGCTTCGGTATGTCCTTCCTGGCTTTTCATGATGGCCATCCTT 396

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Qy 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
Db 397 GGCATGAATGCACAGGTGCACGGGGACATGAGAAGGTGAGGCTCACATTCTGCTG 456

Qy 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal 140
Db 457 ACGGCTGGAATCATCTTCATCATCACGGGCATGTGTGTCTCATCCTGTGAGCTGGGT 516

Qy 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
Db 517 GCCAATGCATCATCAGAGATTTCATTAATCAATAGTAATGTTGCCCAAAACGTGAG 576

Qy 161 LeuGlyGluAlaLeuTyrIleuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
Db 577 CTTGGAGAAAGCTCTCTACTTAGATGACACCGGCACCTGGTCTGATTTGTTGGAGGAGCT 636

Qy 181 LeuPheCysCysValPheCysAsnGlnLysSerSerSerTyrArgTyrSerIlePro 200
Db 637 CTGTTCTGCTGCGTTTTTTTGTTCACGAAAGACAGTAGCTACAGATACCTCGATACCT 696

Qy 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
Db 697 TCCCATCGACACAAACCAAAAGATTATCACCCGGAAGAGTCACCGAGCGTCTACTCC 756

Qy 221 ArgSerGlnTyrVal 225
Db 757 AGAAGTCAGTATGTG 771

RESULT 11
US-10-201-853-357
; Sequence 357, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 357
; LENGTH: 2010

```

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-357

Alignment Scores:
Pred. No.: 1,54e-149 Length: 2010
Score: 1172.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-732-120 (1-225) x US-10-201-853-357 (1-2010)

QY 1 MetAlaThrHisAlaLeuGluLeuAlaGlyLeuPheLeuGlyGlyValGlyMetValGly 20
DB 97 ATGGCAACCATCCCTAGAAATCGCTGGGCTGTTCTTGGTGGTGTGAATGGTGGG 156
QY 21 ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnAsnIle 40
DB 157 ACAGTGGCTGCTACTGTCATGCCCTCAGTGAGAGTGTGGCCCTTCATTGAAAAACAATC 216
QY 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60
DB 217 GTGGTGTGTTGAAAAATCTATGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
QY 61 ArgMetGlnCysLysIleTyrAspSerLeuAlaLeuSerPheLeuAlaPheMetMetAlaIle 100
DB 277 AGGATGCAGTGCAGAAATCTATGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
QY 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu 100
DB 337 AGAGGACTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
QY 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
DB 397 GGCATGAAATGCACAGGTGCACGGGGCAATGAGAGGTGAGGCTCAGATTCGCTGCTGCTG 456
QY 121 ThrAlaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerIlePro 140
DB 457 ACGGCTGGATCATCTTTCATCATCATCGGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516
QY 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160
DB 517 GCCAATGCCATCATCAGAGATTTCTATACTCAATAGTGAATGTGCCAAAAACGTGAG 576
QY 161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrAlaLeuValLeuIleValGlyGlyAla 180
DB 577 CTGGAGAAAGCTCTCTACTTAGGATGACACCGCATCTGGTGTGCTGCTGCTGCTGCTGCTG 636
QY 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerTyrArgTyrSerIlePro 200
DB 637 CTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
QY 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220
DB 697 TCCCATCGCACACCCAAAAAGTTATCACCCGAAAGAGTACACCGAGGCTCTACTCC 756
QY 221 ArgSerGlnTyrVal 225
DB 757 AGAAGTCAGTATGTG 771

RESULT 12
US-10-063-745-119
; Sequence 119, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geiritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

RESULT 13

US-10-063-512-119
 ; Sequence 119, Application US/10063512
 ; Publication No. US20030018183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,512
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 119
 ; LENGTH: 2010
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-512-119

Alignment Scores:

Pred. No.:	1,54e-149	Length:	2010
Score:	1172.00	Matches:	225
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-063-732-120 (1-225) x US-10-063-512-119 (1-2010)

QY	1	MetAlaThrHisAlaLeuGluAlaGlyLeuPheLeuGlyValGlyMetValGly	20
DB	97	ATGGCAACCCATGCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGGATGTGGGC	156
QY	21	ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle	40
DB	157	ACAGTGGCTGTCACTGTCTATGCTCAGTGGAGAGTGTGGCTTCATTGAAACCAACATC	216
QY	41	ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle	60
DB	217	GTGGTTTTTGAAATCTCTGGGAAGGACTGTGGATGAATTGGTGGAGGCTTAACATC	276
QY	61	ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla	80
DB	277	AGGATGCAGTGCMAAATCTATGATTCCTCGTGGCTCTTTCTCCGGACCTACAGCAGCC	336
QY	81	ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	100
DB	337	AGAGGACTGATGTGTGCTTCCTCGTATGTCCTTCTGGCTTCATGATGCCATCCCT	396
QY	101	GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu	120
DB	397	GGCATGAATGCACAGGTGCACGGGGACAAATGAGAGGTTGAAGGCTCAATTCCTGCTG	456
QY	121	ThrAlaGlyIleIlePheIleThrGlyMetValValLeuIleProValSerTrpVal	140
DB	457	ACGGCTGAATCATCTTCATCATACAGGGCATGGTGGTGGCTCATCTCTGAGCTGGGT	516
QY	141	AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu	160
DB	517	GCCATGTCATCATCAGAGATTCATAAATCAATAGTAGAATGTTGCCAAAAAGTGGAG	576
QY	161	LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla	180
DB	577	CTTGAGAGGCTCTCTACTTAGGATGGACCGGACCTGGTGTGCTGATTTGTTGGAGGCT	636

QY	181	LeuPheCysCysValPheCysAsnGluLysSerSerTyrArgTyrSerIlePro	200
DB	637	CTGTTCTGCTGCTGTTTTTTTGTGCAACGAAAGACAGTAGCTACAGATACCTACCT	696
QY	201	SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer	220
DB	697	TCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAGTCAACGAGCGCTACTCC	756
QY	221	ArgSerGlnTyrVal	225
DB	757	AGAGTCAAGTATGTG	771

RESULT 14

US-10-063-513-119
 ; Sequence 119, Application US/10063513
 ; Publication No. US20030018172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,513
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 119
 ; LENGTH: 2010
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-513-119

Alignment Scores:

Pred. No.:	1,54e-149	Length:	2010
Score:	1172.00	Matches:	225
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-063-732-120 (1-225) x US-10-063-513-119 (1-2010)

QY	1	MetAlaThrHisAlaLeuGluAlaGlyLeuPheLeuGlyValGlyMetValGly	20
DB	97	ATGGCAACCCATGCTTAGAAATCGCTGGCTGTTCTTGGTGGTGTGGATGTGGGC	156
QY	21	ThrValAlaValThrValMetProGlnTrpArgValSerAlaPheIleGluAsnIle	40
DB	157	ACAGTGGCTGTCACTGTCTATGCTCAGTGGAGAGTGTGGCTTCATTGAAACCAACATC	216
QY	41	ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle	60
DB	217	GTGGTTTTTGAAATCTCTGGGAAGGACTGTGGATGAATTGGTGGAGGCTTAACATC	276
QY	61	ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla	80
DB	277	AGGATGCAGTGCMAAATCTATGATTCCTCGTGGCTCTTTCTCCGGACCTACAGCAGCC	336
QY	81	ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	100
DB	337	AGAGGACTGATGTGTGCTTCCTCGTATGTCCTTCTGGCTTCATGATGCCATCCCT	396
QY	101	GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu	120
DB	397	GGCATGAATGCACAGGTGCACGGGGACAAATGAGAGGTTGAAGGCTCAATTCCTGCTG	456

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2004, 16:52:13 ; Search time 41 Seconds
(without alignments)
1731.502 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGLFLGVMGVG.....QKSYHTGKKSPVRSQYV 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	664.5	56.7	224 11	Q8BXA6	Q8BXA6 mus musculus
2	538	45.9	213 13	Q805G0	Q805G0 xenopus lae
3	538	45.9	214 13	Q98SR2	Q98SR2 gallus gall
4	538	45.9	214 13	Q90XQ9	Q90XQ9 xenopus lae
5	533	45.5	214 13	Q9DB12	Q9DB12 xenopus lae
6	523.5	44.7	209 13	Q90XR8	Q90XR8 brachydanio
7	522.5	44.6	215 13	Q90XR8	Q90XR8 brachydanio
8	517.5	44.2	216 13	Q90XR0	Q90XR0 gallus gall
9	517.5	44.1	214 13	Q90XR0	Q90XR0 brachydanio
10	514	43.9	214 13	Q7T2P4	Q7T2P4 brachydanio
11	503	42.9	210 13	Q90XR4	Q90XR4 brachydanio
12	497.5	42.4	218 13	Q90XR2	Q90XR2 brachydanio
13	491	41.9	219 11	Q810I9	Q810I9 mus musculus
14	483.5	41.3	206 13	Q90XS1	Q90XS1 brachydanio
15	477.5	40.7	266 4	Q8NWJ3	Q8NWJ3 homo sapien
16	435	37.1	213 13	Q7ZS22	Q7ZS22 xenopus lae

17	431	36.8	199	4	Q7Z4Y7	Q7Z4Y7 homo sapien
18	430	36.7	211	4	Q7Z4X9	Q7Z4X9 homo sapien
19	425.5	36.3	211	13	Q90XR6	Q90XR6 brachydanio
20	422	36.0	211	13	Q8AVG4	Q8AVG4 xenopus lae
21	403.5	34.4	199	13	Q7ZTS2	Q7ZTS2 brachydanio
22	399.5	34.1	210	13	Q90XQ8	Q90XQ8 brachydanio
23	382	32.6	237	13	Q90XS0	Q90XS0 brachydanio
24	362	30.9	222	13	Q7T2E7	Q7T2E7 brachydanio
25	336.5	28.7	140	6	Q7YS66	Q7YS66 sus scrofa
26	329	28.1	226	4	Q96N78	Q96N78 homo sapien
27	308.5	26.3	220	11	Q9D7U6	Q9D7U6 mus musculus
28	305.5	26.1	236	13	Q8QHA3	Q8QHA3 brachydanio
29	304	25.9	229	11	Q9CX57	Q9CX57 mus musculus
30	296.5	25.3	264	11	Q8BZS5	Q8BZS5 mus musculus
31	283	24.1	219	13	Q90XE7	Q90XE7 brachydanio
32	281	24.0	236	13	Q7T021	Q7T021 brachydanio
33	280.5	23.9	178	4	Q8N7P3	Q8N7P3 homo sapien
34	240.5	20.5	224	5	Q9N9W1	Q9N9W1 halocynthia
35	240.5	20.5	224	5	Q9N9W2	Q9N9W2 halocynthia
36	224	19.1	100	6	Q7YS67	Q7YS67 sus scrofa
37	217	18.5	193	11	Q8VC62	Q8VC62 mus musculus
38	194	16.6	194	13	Q7T018	Q7T018 brachydanio
39	176.5	15.1	296	11	Q9D7D7	Q9D7D7 mus musculus
40	168.5	14.4	235	6	Q9TUF7	Q9TUF7 bos taurus
41	155.5	13.3	256	13	Q90XR5	Q90XR5 brachydanio
42	148	12.6	159	13	Q8QFL7	Q8QFL7 brachydanio
43	134	11.4	341	13	Q90XE1	Q90XE1 brachydanio
44	134	11.4	341	13	Q90XR3	Q90XR3 brachydanio
45	131	11.2	185	13	Q7T020	Q7T020 brachydanio

ALIGNMENTS

RESULT 1

Q8BXA6	PRELIMINARY;	PRT;	224 AA.
ID	Q8BXA6		
AC	Q8BXA6;		
DT	01-MAR-2003 (TRENBLrel. 23, Created)		
DT	01-MAR-2003 (TRENBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	Similar to claudin-17.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Head;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium.		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573(2002).		
DR	EMBL; AK048287; BAC33296.1; -		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005923; C:tight junction; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	InterPro; IPR006187; Claudin.		
DR	InterPro; IPR006188; Claudin reg.		
DR	Pfam; PF00822; PMP22 Claudin.		
DR	PRINTS; PR01077; CLAUDIN.		
DR	PROSITE; PS01346; CLAUDIN.		
SQ	SEQUENCE 224 AA; 24653 MW; 6E049CE63AB60A34 CRC64;		
Query Match 56.7%; Score 664.5; DB 11; Length 224;			
Best Local Similarity 54.7%; Pred. No. 3.1e-36;			
Matches 123; Conservative 39; Mismatches 62; Indels 1; Gaps 1;			
QY	1 MATHALEIAGLFLGVMGVGTVAVTWMPQWVSFAFTENNIVVFENFEGLMWNCVQANI 60		

Db 1 MAFYPLQIAGLVLPFGVLGVTIGTLLPQWRVSAFIGSNIIIFIRIWEGLMNCICQAMV 60
QY 61 RMQCKIYDLSLALSPDLQARGLMCAASVMSFLAFMAILGMKTRCTGDNKVKAHILL 120
Db 61 TFQCKFYNSILAPVLEAARALMCVAVALLVIGICGMKQLQCTGSSSRVKAYLIG 120
QY 121 TAGIIFITGMVLIPVSWANAIIRDVNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TSGVILFITGMVLIPVSWANAIIRDVNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCNCKSSRYSPSHRTTQKSYHTGKSPSVYSRQYV 225
Db 181 LLLCGYCCCNKRWHRYPVPAYRVPQDNQRNVTVPRKSTSV 224

RESULT 2

Q805G0 PRELIMINARY; PRT; 213 AA.
AC Q805G0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Claudin4L2.
GN CLDN4L2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of xenopus embryos.";
RL Gene Expr. Patterns 2:23-26(2002).
DR EMBL; AB072909; BAC21014.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN.
SQ SEQUENCE 213 AA; 22913 MW; ACF10FC95F9C16A1 CRC64;

Query Match 45.9%; Score 538; DB 13; Length 213;
Best Local Similarity 45.8%; Pred. No. 1.3e-45;
Matches 103; Conservative 43; Mismatches 67; Indels 12; Gaps 4;
QY 1 MATHALIEAGLVGGMVGVTVVMPQWVSFAFIENNIIVFENFWEGLMNCVQANI 60
Db 1 MASTGLQLGLMALIGVWGCIITCALPFWMRVTAFIGNIIVVAQTIWEGLMNCIVOSTG 60
QY 61 RMQCKIYDLSLALSPDLQARGLMCAASVMSFLAFMAILGMKTRCTGDNKVKAHILL 120
Db 61 QMCKVYDLSLALSPDLQARGLMCAASVMSFLAFMAILGMKTRCTGDNKVKAHILL 119
QY 121 TAGIIFITGMVLIPVSWANAIIRDVNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 120 VSGIVFLVAGILLIPVCSANSIIRDVNSIVNVAQKRELGEALYLGWTTALVIVGGA 179
QY 181 LFCVFCNCKSSRYSPSHRTTQKSYHTGKSPSVYSRQYV 225
Db 180 LLCC--SCPKREDNH--YS-----AQYTAASQPRSDPSKNYV 213

RESULT 3

Q98SR2 PRELIMINARY; PRT; 214 AA.
ID Q98SR2
AC Q98SR2
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Claudin-3.
GN CLDN3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Reardon E., Kojima S., Rizzolo L.J.;
RT "Sequence of chick claudin-3 cDNA.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334677; AAK20876.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR Pfam; PF00822; PMP22 Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN.
SQ SEQUENCE 214 AA; 23090 MW; A2540116CBD53978 CRC64;
Query Match 45.9%; Score 538; DB 13; Length 214;
Best Local Similarity 48.6%; Pred. No. 1.3e-45;
Matches 107; Conservative 38; Mismatches 65; Indels 10; Gaps 4;
QY 6 LEIAGLVGGMVGVTVVMPQWVSFAFIENNIIVFENFWEGLMNCVQANIRMOCK 65
Db 5 LEIGGVALSIVLWLCISICCALPFWMRVTAFIGNIIVVAQTIWEGLMNCVQSTGQMOCK 64
QY 66 IYDLSLALSPDLQARGLMCAASVMSFLAFMAILGMKTRCTGDNKVKAHILLTAGII 125
Db 65 VYDLSLALSPDLQARGLMCAASVMSFLAFMAILGMKTRCTGDNKVKAHILLTAGII 123
QY 126 FIITGMVLIPVSWANAIIRDVNSIVNVAQKRELGEALYLGWTTALVIVGALPCCV 185
Db 124 FLISGIMTLIPVSWANSIIRDVNSIVNVAQKRELGTSLVGVMAASALLFGGALLCC- 182
QY 186 FCNCKSSRYSPSHRTTQKSYHTGKSPSVYSRQYV 225
Db 183 -SCPPKDERY---APS----KVAYSAPRSVTSYDKRNV 214
RESULT 4
Q90XQ9 PRELIMINARY; PRT; 214 AA.
ID Q90XQ9
AC Q90XQ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Claudin A (Claudin4L1).
GN CLDN A OR CLDN4L1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26(2002).

GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006187; Claudin_reg.
DR InterPro; IPR006188; Claudin.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 44.2%; Score 517.5; DB 13; Length 216;
Best Local Similarity 45.0%; Pred. No. 1.4e-43;
Matches 95; Conservative 43; Mismatches 70; Indels 3; Gaps 2;

QY 1 MATHALEIAGLFLGGVGVGTAVTVMPOWRVSAFTENNVFENFEGLMWNCVQANI 60
DB 1 MASAAVEILGLGLGWVILACGLPMQVSAFIDVNIIVVQATINEGLMNCVQSTG 60

QY 61 RMCKIYDLSLLALSPDQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
DB 61 QMCKVYDLSLLALRPEVQAGRALTVIVALLGLVALMTVVGAQCTNCIRPG-KMKSRIVI 119

QY 121 TAGIIFIITGMVLPVSWANAIIRDFYNSIVNVAQKREIGALYLGWTTALVLIVGGA 180
DB 120 AGTTIILGVLVPLCFWAFANIVISDFYDPSPPSKREIGAALYIIGWAATALLFGGC 179

QY 181 LFCVFCCKEKKSSY--RYSIPSHRTQKSY 209
DB 180 LCCSCCLQRDETSTFPVKYSAPRRPTSGEY 210

RESULT 9
Q90XR0 PRELIMINARY; PRT; 214 AA.
ID Q90XR0
AC Q90XR0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Claudin h.
GN CLDNH.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia."
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359434; AAJ01841.1; -.
DR ZFIN; ZDB-GENE-010328-8; clnhd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 22788 MW; 38163AB7E50BF058 CRC64;

Query Match 44.1%; Score 517; DB 13; Length 214;
Best Local Similarity 44.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 45; Mismatches 68; Indels 10; Gaps 3;

QY 6 LEIAGLFLGGVGVGTAVTVMPOWRVSAFTENNVFENFEGLMWNCVQANIRMOCK 65
DB 5 LEIGALGIGIIGIISIVACALPMWRVSAFVGANIVTAQVIEGLMNCVQSTGQWCK 64

QY 66 IYDLSLLALSPDQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILLTAGII 129


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Db      65 VYDSMLALGQDLQASRAMTVIAILLAVLGWMSVWGAKCTNCIED-EGAKAKWIVVSGIM 123
QY      126 FIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIVGALFCCV 185
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      124 FIITGMVVLIPVSAWVAQIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIVGALFCCV 183
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      186 FCCNEKSSSYRYSIPSHRTQKSYHTGKKSPPSVYSRSQV 225
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      184 --CPPKEKKY-----KPARMGYSAPRSASAGYDKDYV 214
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
Q7T2P4 PRELIMINARY; PRT; 214 AA.
AC Q7T2P4;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Claudin h.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053223; AAH53223.1; -.
SQ SEQUENCE 214 AA; 2792 MW; D896FD3E50DF518 CRC64;

Query Match 43.9%; Score 514; DB 13; Length 214;
Best Local Similarity 43.6%; Pred. No. 3.2e-43;
Matches 96; Conservative 46; Mismatches 68; Indels 10; Gaps 3;

QY      6 LEIAGLGLGGVGMGTVAIVTMQWRVSATFENNIVVFENFWEGLMNCVQANIRMOCK 65
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      5 LEIGGIALGIGWITISVACALPMWRVSATFENIVTAQVMDGLMNCVQSGQMOCK 64
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      66 IYDSLLALSPLDQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILLTAGI 125
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      65 VYDSMLALGQDLQASRAMTVIAILLAVLGWMSVWGAKCTNCIED-EGAKAKWIVVSGIM 123
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      126 FIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIVGALFCCV 185
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      124 FIITGMVVLIPVSAWVAQIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIVGALFCCV 183
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      186 FCCNEKSSSYRYSIPSHRTQKSYHTGKKSPPSVYSRSQV 225
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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Db      184 --CPPKEKKY-----KPARMGYSAPRSASAGYDKDYV 214
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 11
Q90XR4 PRELIMINARY; PRT; 210 AA.
AC Q90XR4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Claudin j.
GN CLDNJ.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201 (2001).
DR EMBL; AF359430; AAL01837.1; -.
DR ZFIN; ZDB-GENE-010328-10; cldnj.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 210 AA; 22895 MW; F9A6964463E55775 CRC64;

Query Match 42.9%; Score 503; DB 13; Length 210;
Best Local Similarity 43.0%; Pred. No. 3.9e-42;
Matches 95; Conservative 47; Mismatches 67; Indels 12; Gaps 4;

QY      5 ALEIAGLGLGGVGMGTVAIVTMQWRVSATFENNIVVFENFWEGLMNCVQANIRMOCK 64
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      2 ALQVLGITLSMIGFAGIIICALLPMWKVTAFIGTNIVVAQVFWGLMNTCYERIGQMOC 61
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      65 KIYDSLLALSPLDQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILLTAGI 124
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      62 KLYDALLDLDPFLOASRGLIVTMMALASLAFLEIGADCTNCL-SNPRAGRIVVSGI 120
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      125 IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGTWTTALVLIVGALFCC 184
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      121 TFLMSGUUTTVPVSWTADSIIRDFNPNVHEALKREMGALYVGMWLTAGFLVFGAILCT 180
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      185 VFCNEKSSSYRYSIPSHRTQKSYHTGKKSPPSVYSRSQV 225
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      181 --SCPERDNY---LPRYTLTKSTHSG-----YAVKNYV 210
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
Q90XR2 PRELIMINARY; PRT; 218 AA.
AC Q90XR2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Claudin c.
GN CLDNC.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359432; AAL01839.1; -.
DR ZFIN; ZDB-GENE-010328-3; cldnc.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
SQ SEQUENCE 218 AA; 23425 MW; 82CA23D13306110F CRC64;

Query Match 42.4%; Score 497.5; DB 13; Length 218;
Best Local Similarity 42.7%; Pred. No. 1.5e-41;
Matches 96; Conservative 48; Mismatches 74; Indels 7; Gaps 5;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSARFNIENNIVVFENFWEGLMNCVQANI 60
Db 1 MASFGLEIAGLVTLVGLNLTINIVCCALPMWRVTFGTIVTAQVTWEGIMNSCVQSTG 60

QY 61 RMCKIYDLSLALSPDLOAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
Db 61 QMCKVYDLSLALPDLOAARALCVVTLIVLGLVLDAGAKCTTCVEDRNS-KSRLVL 119

QY 121 TAGIIFIITGMVLIIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLIIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCVFCNCKSSSYRISPSHRTTKQSYHTGKKSPSVYSRQYV 225
Db 180 LLCCA-CSSGGTQGRHMACYSTSVPH----SRGPPPYPTKNYV 219

SQ SEQUENCE 218 AA; 23425 MW; 82CA23D13306110F CRC64;

Query Match 41.3%; Score 483.5; DB 13; Length 206;
Best Local Similarity 47.5%; Pred. No. 3.4e-40;
Matches 87; Conservative 40; Mismatches 55; Indels 1; Gaps 1;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSARFNIENNIVVFENFWEGLMNCVQANI 60
Db 1 MVSAGLQMGVIALAVIGMIGVIVVLCILPMMQVTAFIGQNIIVTAQVTWEGIMNSCVQSTG 60

QY 61 RMCKIYDLSLALSPDLOAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
Db 61 QMCKVYDLSLALSPDLOAARALCVVTLIVLGLVLDAGAKCTTCIXE-ERAKAKVCV 119

QY 121 TAGIIFIITGMVLIIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 120 ISGAIFIVAGVLCILPVCWTANNIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFC 183
Db 180 LLC 182

RESULT 15
QBWUW3 PRELIMINARY; PRT; 266 AA.
AC Q8WUW3
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359423; AAL01830.1; -.
DR ZFIN; ZDB-GENE-010328-1; cldna.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
SQ SEQUENCE 206 AA; 21694 MW; 59CF7A8554A2EFCF CRC64;

Query Match 41.3%; Score 483.5; DB 13; Length 206;
Best Local Similarity 47.5%; Pred. No. 3.4e-40;
Matches 87; Conservative 40; Mismatches 55; Indels 1; Gaps 1;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSARFNIENNIVVFENFWEGLMNCVQANI 60
Db 1 MVSAGLQMGVIALAVIGMIGVIVVLCILPMMQVTAFIGQNIIVTAQVTWEGIMNSCVQSTG 60

QY 61 RMCKIYDLSLALSPDLOAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
Db 61 QMCKVYDLSLALSPDLOAARALCVVTLIVLGLVLDAGAKCTTCIXE-ERAKAKVCV 119

QY 121 TAGIIFIITGMVLIIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 120 ISGAIFIVAGVLCILPVCWTANNIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFC 183
Db 180 LLC 182

RESULT 14
Q90XS1 PRELIMINARY; PRT; 206 AA.
AC Q90XS1;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Claudin a.
GN CLDNA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359423; AAL01830.1; -.
DR ZFIN; ZDB-GENE-010328-1; cldna.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
SQ SEQUENCE 206 AA; 21694 MW; 59CF7A8554A2EFCF CRC64;

Query Match 41.3%; Score 483.5; DB 13; Length 206;
Best Local Similarity 47.5%; Pred. No. 3.4e-40;
Matches 87; Conservative 40; Mismatches 55; Indels 1; Gaps 1;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSARFNIENNIVVFENFWEGLMNCVQANI 60
Db 1 MVSAGLQMGVIALAVIGMIGVIVVLCILPMMQVTAFIGQNIIVTAQVTWEGIMNSCVQSTG 60

QY 61 RMCKIYDLSLALSPDLOAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
Db 61 QMCKVYDLSLALSPDLOAARALCVVTLIVLGLVLDAGAKCTTCIXE-ERAKAKVCV 119

QY 121 TAGIIFIITGMVLIIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 120 ISGAIFIVAGVLCILPVCWTANNIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFC 183
Db 180 LLC 182

RESULT 13
Q81019 PRELIMINARY; PRT; 219 AA.
AC Q81019;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Claudin 6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Blastocyst;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050138; AAH50138.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 219 AA; 23398 MW; 0300687FAB687E1F CRC64;

Query Match 41.9%; Score 491; DB 11; Length 219;
Best Local Similarity 43.6%; Pred. No. 6.5e-41;
Matches 98; Conservative 43; Mismatches 78; Indels 6; Gaps 3;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSARFNIENNIVVFENFWEGLMNCVQANI 60
Db 1 MASTGLQILGIVLITLIGWYNALVSCALPMWRKVTAFIGNSIVVAQMVMWEGIMNSCVQSTG 60

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Search completed: September 1, 2004, 16:55:38
Job time : 42 secs

Search completed: September 1, 2004, 16:55:38
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:52:38 ; Search time 18 Seconds
(without alignments)
645.325 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 1172
Sequence: 1 MATHALEIAGFLGGMVG.....OKSVHTGKSPSVRSQYV 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534	45.6	220	4	US-09-603-552-13
2	530	45.2	113	4	US-09-621-976-5695
3	489	41.7	247	4	US-09-130-491-15
4	479	40.9	202	4	US-09-205-258-344
5	477.5	40.7	218	4	US-09-130-491-14
6	477.5	40.7	218	4	US-09-489-847-209
7	470	40.1	225	4	US-09-673-395A-354
8	439	37.5	211	4	US-09-130-491-4
9	439	37.5	211	4	US-09-603-552-12
10	439	37.5	211	4	US-09-886-683A-4
11	372.5	31.8	230	4	US-09-663-600A-186
12	363.5	31.0	230	4	US-09-663-600A-92
13	310.5	26.5	264	4	US-09-724-864-64
14	296	25.3	228	4	US-09-603-552-1
15	294	25.1	137	3	US-09-188-930-174
16	294	25.1	137	4	US-09-312-283C-174
17	204	17.4	99	4	US-09-621-976-4220
18	201	17.2	207	1	US-08-557-917A-2
19	201	17.2	207	3	US-09-084-153-2
20	201	17.2	207	3	US-09-084-079-2
21	190	16.2	218	3	US-09-084-079-5
22	143	12.2	72	4	US-09-489-847-366
23	143	12.2	73	4	US-09-489-847-241
24	115	9.8	323	4	US-09-123-030-8
25	108	9.2	32	4	US-09-205-258-872
26	92.5	7.9	831	2	US-08-677-734A-11
27	92.5	7.9	831	4	US-09-097-053-11

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28 91.5 7.8 445 4 US-09-328-352-6669 Sequence 6669, Ap
29 87.5 7.5 834 2 US-08-677-734A-9 Sequence 9, Appl
30 87.5 7.5 834 2 US-08-677-734A-10 Sequence 10, Appl
31 87.5 7.5 834 4 US-09-097-053-9 Sequence 9, Appl
32 87.5 7.5 834 4 US-09-097-053-10 Sequence 10, Appl
33 85.5 7.3 832 2 US-08-677-734A-12 Sequence 12, Appl
34 85.5 7.3 832 4 US-09-097-053-12 Sequence 12, Appl
35 85 7.3 157 2 US-08-883-070-3 Sequence 3, Appl
36 83 7.1 548 3 US-08-903-139B-28 Sequence 28, Appl
37 81.5 7.0 315 4 US-09-123-030-10 Sequence 10, Appl
38 81 6.9 159 4 US-09-134-001C-4062 Sequence 4062, Ap
39 81 6.9 327 3 US-09-392-014-2 Sequence 2, Appl
40 80 6.8 223 4 US-09-266-764-2 Sequence 2, Appl
41 80 6.8 327 4 US-09-123-030-12 Sequence 12, Appl
42 79.5 6.8 422 4 US-09-489-039A-7295 Sequence 7295, Ap
43 79.5 6.8 472 4 US-09-934-899-10 Sequence 10, Appl
44 79 6.7 22 4 US-09-205-258-869 Sequence 869, App
45 79 6.7 263 4 US-09-134-000C-5703 Sequence 5703, Ap

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ALIGNMENTS

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RESULT 1
US-09-603-552-13
; Sequence 13, Application US/09603552
; Patent No. 6590089
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
; FILE REFERENCE: PC-0016 US
; CURRENT APPLICATION NUMBER: US/09/603,552
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank No. 6590089 g2570129
US-09-603-552-13

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Query Match 45.6%; Score 534; DB 4; Length 220;
Best Local Similarity 46.2%; Pred. No. 9.2e-52;
Matches 104; Conservative 35; Mismatches 72; Indels 14; Gaps 4;

QY 6 LEIAGFLGGVGMGTVAVTVPQVRSYAFIENNVVFENFWEGLWNCVROAIRMOCK 65
Db 5 LEITGTALAVLWGLTIVCCALPMWRVSFIQNIITSQNIWEGLWNCVQSTGQMOCK 64
QY 66 IYDLSLALSPDLOAAGLMCAASVFLAFPMALIGMKTCTGCDNEKVKAHILLTAGII 125
Db 65 VYDLSLALPDQAARALIIVALLAAGLLVAVGACQNCVQD-DTAKAKITIVAGVL 123
QY 126 FIITGMVILIPVSWANAIIRDYFNVSVAQKRELGALYLGWTTALVIVGGALFCCV 185
Db 124 FLAALITLIPVSWSANIIRDYFNVPVPAQKREAGLYVGVAAALQLLGGALLCC- 182
QY 186 FCCNEKSSSYR-----YSTPSHRTTOKSVHTGKKSFSVRSQYV 225
Db 183 -SCPPEKKYATKVYVSAPRSTGPGASLTGTG-----YDRKDYV 220

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RESULT 2

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US-09-621-976-5695
; Sequence 5695, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5695
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: -79...-1
NAME/KEY: UNSURE
LOCATION: 25
OTHER INFORMATION: Xaa = *, Ser
US-09-621-976-5695

Query Match 45.2%; Score 530; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLEFGVGMGTAVTVMPOWRVSAPFIENNVFENFWGLMNCVQANI 60
DB 1 MATHALEIAGLEFGVGMGTAVTVMPOWRVSAPFIENNVFENFWGLMNCVQANI 60

QY 61 RMCKLYDLSLLSPDLQAARGLMCAASVMSFLAFWAILGMK 103
DB 61 RMCKLYDLSLLSPDLQAARGLMCAASVMSFLAFWAILGMK 103

RESULT 3
US-09-130-491-15
Sequence 15, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-130-491-15

Query Match 41.7%; Score 489; DB 4; Length 247;
Best Local Similarity 42.6%; Pred. No. 1.2e-46;
Matches 100; Conservative 41; Mismatches 72; Indels 22; Gaps 4;

QY 5 ALETAGLFLGGVGMGTAVTVMPOWRVSAPFIENNVFENFWGLMNCVQANIRMQC 64
DB 4 SLEITGSLAVLGMCTIVCCALPMWRVSAPFIENNVFENFWGLMNCV-QSTGQMOC 62

QY 65 KIYDLSLLSPDLQAARGLMCAASVMSFLAFWAILGMKCTCTGDNKVKAHILLTAGI 124
DB 63 KMVDSLLALPQDLQAARALIVVLSILAAFLGLVALVGAQCTNCVQD-ETAKAKITIVAGV 121

QY 125 IFITGMVLLTPSVWANAIRDFNSVNVVAQKRELGEALYLGWTTALVILVGGALPCC 184
DB 122 LFLAAVLLTPVFSVNSANTIIRDFNPLVPEAKREMGTLGVVMAAALQLGGLLCC 181

QY 185 VFCNCKSSSYR--YSIP-----SHRTTQKSYHTGKSPSVY 219

DB 182 SCPPEKYAPTKILYSAPRSTGPGTGTAYDKRTTSRPGARTPHHHHYSMY 236

RESULT 4
US-09-205-258-344
Sequence 344, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (202)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-344

Query Match
Best Local Similarity 40.9%; Score 479; DB 4; Length 202;
Matches 88; Conservative 43; Mismatches 55; Indels 6; Gaps 3;

QY 10 GLFLGGVGVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVROANIRMOCKIYDS 69
Db 2 GIALAVLGNLAVMLCCALPMWRVTFAGSNIVTSQTIWGLMNCVQSTGCMOCKVYDS 61

QY 70 LLALSPDLQAARGLMCAASVMSFLAFMWAILGMKCTRCTGNEKVKAHILLTAGILIRIT 129
Db 62 LLALPQDLQAARALVIISIIAVALGVLLSVGGKCTNCLED-ESAKAKTMIVAGVWFLA 120

QY 130 GMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGTTALVLIIVGGALFCCVFC- 188
Db 121 GLMVIVPVSHTAHNIIQDFYNPLVASGQKREMGASLYVGNAAAGLLLLGGGLCC--NCP 178

QY 189 --NEKSSSYRS 198
Db 179 PRTDKPYSAKYS 190

RESULT 5
US-09-130-491-14
; Sequence 14, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 218

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; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-130-491-14

Query Match
Best Local Similarity 40.7%; Score 477.5; DB 4; Length 218;
Matches 94; Conservative 45; Mismatches 75; Indels 15; Gaps 5;

QY 1 MATHALEIAGLFLGGVGVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVROANI 60
Db 1 MGSAALEILGLVLCVLGNGGLIILACGLPMQVTFADHNIIVTAQTITWGLMNCVQSTG 60

QY 61 RMCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMWAILGMKCTRCTGNEKVKAHILL 120
Db 61 HMCKVYDSVLALSTEVQAARALTYSALLAFVALFVTLAGACCTTCVAPG-PAKARVAL 119

QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGTTALVLIIVGGA 180
Db 120 TGGVLYLFCGLLALVPLCFWAFNIIVREFYDPSVPSQKYLGAALYIGWAATALLMVGGC 179

QY 181 LFCC-VFCCN---EKSSSYRSYRSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 180 LLCGAWVCTGRPDLSPFPVKSAPRRPTA-----TGD-----YDKKNYV 218

RESULT 6
US-09-489-847-209
; Sequence 209, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-209

Query Match
Best Local Similarity 40.7%; Score 477.5; DB 4; Length 218;
Matches 94; Conservative 45; Mismatches 75; Indels 15; Gaps 5;

QY 1 MATHALEIAGLFLGGVGVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVROANI 60
Db 1 MGSAALEILGLVLCVLGNGGLIILACGLPMQVTFADHNIIVTAQTITWGLMNCVQSTG 60

QY 61 RMCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMWAILGMKCTRCTGNEKVKAHILL 120
Db 61 HMCKVYDSVLALSTEVQAARALTYSALLAFVALFVTLAGACCTTCVAPG-PAKARVAL 119

QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGTTALVLIIVGGA 180
Db 120 TGGVLYLFCGLLALVPLCFWAFNIIVREFYDPSVPSQKYLGAALYIGWAATALLMVGGC 179

QY 181 LFCC-VFCCN---EKSSSYRSYRSHRTTQKSYHTGKSPSVYSRSQYV 225
; SEQ ID NO 14
; LENGTH: 218

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Fri Sep 3 10:15:56 2004

us-10-063-732-120.ra1

Db 180 LLCCGAWCTGRPDLSPVKYSAPRRPTA-----TGD-----YDKKNV 218

RESULT 7

US-09-673-395A-354

; Sequence 354, Application US/09673395A

; Patent No. 6620923

; GENERAL INFORMATION:

; APPLICANT: SPECHT, THOMAS

; APPLICANT: HINZMANN, BERNI

; APPLICANT: SCHMITT, ARMIN

; APPLICANT: PILARSKY, CHRISTIAN

; APPLICANT: DAHL, EDGAR

; APPLICANT: ROSENTHAL, ANDRE

; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE

; FILE REFERENCE: ALBRE-12

; CURRENT APPLICATION NUMBER: US/09/673,395A

; CURRENT FILING DATE: 2000-10-17

; NUMBER OF SEQ ID NOS: 637

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 354

; LENGTH: 225

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-673-395A-354

Query Match 40.1%; Score 470; DB 4; Length 225;

Best Local Similarity 40.9%; Pred. No. 1.4e-44;

Matches 92; Conservative 42; Mismatches 77; Indels 14; Gaps 2;

Qy 1 MATHALEIAGLFGGVGMGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVQANI 60

Db 15 MANSGLQLLGFSAALQALGMLCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120

Qy 61 RMCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120

Db 75 MMCKMYDLSLALSAALQALGMLCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 134

Qy 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGA 180

Db 135 GGGIIFIVAGLAALVACSWYGHQIVTDYFNPLIPTNIKYEFGAIFGWAGSALVILGA 194

Qy 181 LFCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQV 225

Db 195 LLSCPCPNESKAGYR-----APRSY-----PKSNSKEYV 225

RESULT 8

US-09-130-491-4

; Sequence 4, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-130-491-4

Query Match 37.5%; Score 439; DB 4; Length 211;

Best Local Similarity 36.9%; Pred. No. 3.8e-41;

Matches 83; Conservative 48; Mismatches 80; Indels 14; Gaps 3;

Qy 1 MATHALEIAGLFGGVGMGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVQANI 60

Db 1 MANSGLQLLGFILAGLWIGAVSTALPQWRIYSIAGDNIIVTAQAMVEGLMNCVQSTG 60

Qy 61 RMCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120

Db 61 QIQCCKVFDLSLNLSTLQATRALMVVGILLGVIAIFVATVGMCKKCLDEDEVQKRMVAV 120

Qy 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGA 180

Db 121 IGGAIIFLAGLAILVATAWYGNRIYQEFYDPMTPVNAARYEFGQALFTGMAAASLCILGGA 180

Qy 181 LFCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQV 225

Db 181 LLCC--SCPRTKTSY----PTPRPYK-----PAPSSGKDYV 211

RESULT 9

US-09-603-552-12

; Sequence 12, Application US/09603552

; Patent No. 6590089

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Tang, Y. Tom

; APPLICANT: Patterson, Chandra

; TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE

; FILE REFERENCE: PC-0016 US

; CURRENT APPLICATION NUMBER: US/09/603,552

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PERL Program

; SEQ ID NO 12

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6590089 2057608CD1

US-09-603-552-12

Query Match 37.5%; Score 439; DB 4; Length 211;

Best Local Similarity 36.9%; Pred. No. 3.8e-41;

Matches 83; Conservative 48; Mismatches 80; Indels 14; Gaps 3;

Qy 1 MATHALEIAGLFGGVGMGTVAVTMPQWRVSAFIENNIIVFENFWEGLMNCVQANI 60

Db 1 MANSGLQLLGFILAGLWIGAVSTALPQWRIYSIAGDNIIVTAQAMVEGLMNCVQSTG 60

Qy 61 RMCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120

Db 61 QIQCCKVFDLSLNLSTLQATRALMVVGILLGVIAIFVATVGMCKKCLDEDEVQKRMVAV 120

Qy 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGA 180

Db 121 IGGAIIFLAGLAILVATAWYGNRIYQEFYDPMTPVNAARYEFGQALFTGMAAASLCILGGA 180

Qy 181 LFCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQV 225

Db 181 LLCC--SCPRTKTSY----PTPRPYK-----PAPSSGKDYV 211

RESULT 10

US-09-886-683A-4

; Sequence 4, Application US/09886683A

; Patent No. 6627439

; GENERAL INFORMATION:

; APPLICANT: Hoevel, Thorsten

; APPLICANT: Koch, Stefan

; APPLICANT: Kubbies, Manfred

; APPLICANT: Mundigl, Olaf

; APPLICANT: Rueger, Petra

; TITLE OF INVENTION: Antibodies against SEMP1 (p23)

FILE REFERENCE: Case 20692
CURRENT APPLICATION NUMBER: US/09/886,683A
BEST LOCAL SIMILARITY 31.8%; Score 372.5; DB 4; Length 230;
Best Local Similarity 33.8%; Pred. No. 1.2e-33;
Matches 79; Conservative 55; Mismatches 87; Indels 13; Gaps 5;
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: EP00113344.6
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: EP01107799.7
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-683A-4

Query Match 37.5%; Score 439; DB 4; Length 211;
Best Local Similarity 36.9%; Pred. No. 3.8e-41;
Matches 83; Conservative 48; Mismatches 80; Indels 14; Gaps 3;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOKRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MANAGLQLLGFILAFGLGIGAIIVTALPQWRIVSYAGDNIVTAQAMVEGLMNCVQSQTG 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCT-RTGDNKVKAHIL 120
Db 61 QIOCKVFDSLNLUSSTLQATRLMVGILGVIAIFVATVGMCKCLEDEDEVQRMNAV 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTALVLIYVGA 180
Db 121 IGGAIPLAGLAIIVATAWGNRIVQEFYDPTVNAVRYEFGQALFTGMAASLILGGA 180
QY 181 LFCVFCCKNEKSSRYISHSRRTQKSYHTGKKSPPSVYRSQYV 225
Db 181 LLCC--SCPRTKTSY----PTPRPK-----PAPSSGKDYV 211

RESULT 11

US-09-663-600A-186
Sequence 186, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 186
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: -24..-1
NAME/KEY: UNSURE
LOCATION: 54..79
OTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-663-600A-186

Query Match 31.0%; Score 363.5; DB 4; Length 230;
Best Local Similarity 33.3%; Pred. No. 1.2e-32;
Matches 78; Conservative 54; Mismatches 89; Indels 13; Gaps 5;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOKRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MASLGLQVLGYILGLLGLLTIVAMLLPSWKTSYVGSIVTAVGFSKGLMWCATHSTG 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCT-RTGDNKVKAHIL 119
Db 61 ITQCDIYSTLLGLPADIXAAQAMMVTSSAIISSLAIIISVVGMCCTVFC--QESRAKDRVA 118

US-09-663-600A-186

Query Match 31.8%; Score 372.5; DB 4; Length 230;
Best Local Similarity 33.8%; Pred. No. 1.2e-33;
Matches 79; Conservative 55; Mismatches 87; Indels 13; Gaps 5;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOKRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MASLGLQVLGYILGLLGLLTIVAMLLPSWKTSYVGSIVTAVGFSKGLMWCATHSTG 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCT-RTGDNKVKAHIL 119
Db 61 ITQCDIYSTLLGLPADIXAAQAMMVTSSAIISSLAIIISVVGMCCTVFC--QESRAKDRVA 118
QY 120 LTAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTALVLIYVGG 179
Db 119 VAGGVFFILGGLLGFIPVAVNLHGLRDFYSPVDSMKFGEIGALYLGIISSLSFSLIAG 178
QY 180 ALFCVFCCKNEK--SSSYRYSISHSRRTQKSYHTGKKSPPSVYRSQYV 225
Db 179 IILC--FSCSSQRNRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYY 230

RESULT 12

US-09-663-600A-92
Sequence 92, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 92
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: -24..-1
NAME/KEY: UNSURE
LOCATION: 54..79
OTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-663-600A-92

Query Match 31.0%; Score 363.5; DB 4; Length 230;
Best Local Similarity 33.3%; Pred. No. 1.2e-32;
Matches 78; Conservative 54; Mismatches 89; Indels 13; Gaps 5;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOKRVSAFIENNVFENFWEGLMNCVRQANI 60
Db 1 MASLGLQVLGYILGLLGLLTIVAMLLPSWKTSYVGSIVTAVGFSKGLMWCATHSTG 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCT-RTGDNKVKAHIL 119
Db 61 ITQCDIYSTLLGLPADIXAAQAMMVTSSAIISSLAIIISVVGMCCTVFC--QESRAKDRVA 118

US-09-663-600A-92

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:53:38 ; Search time 16 Seconds
(without alignments)
1352.693 Million cell updates/sec

Title: US-10-063-732-120

Perfect score: 1172

Sequence: 1 MATHALEIAGLFLGGVGMVG.....OKSVHTGKSPSVRSQYV 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	41.7	280	A39484	androgen-withdrawn
2	100.5	8.6	660	A4432	amino acid transpo
3	99.5	8.5	173	A49182	integral membrane
4	97.5	8.3	459	S10196	NADH2 dehydrogenas
5	95.5	8.1	173	A48300	lens membrane prot
6	94.5	8.1	459	T11489	NADH2 dehydrogenas
7	94	8.0	468	T33784	hypothetical prote
8	93	7.9	484	C75609	amino acid ABC tra
9	92.5	7.9	637	S48921	hypothetical prote
10	92.5	7.9	831	B40204	Na+/H+-exchanging
11	91.5	7.8	988	S37078	chloride channel p
12	89.5	7.6	380	AH0781	probable membrane
13	89	7.6	440	T11358	NADH2 dehydrogenas
14	88	7.5	618	S33044	hypothetical prote
15	87	7.4	297	T23309	hypothetical prote
16	86	7.4	664	S59638	glucose transport
17	87	7.4	664	S59637	glucose transport
18	86.5	7.4	459	T11398	NADH2 dehydrogenas
19	86	7.3	182	T19126	hypothetical prote
20	86	7.3	783	E89551	protein K04E7.2 [i
21	86	7.3	796	T37330	probable low-affin
22	85.5	7.3	486	AC0365	probable permease
23	85.5	7.3	832	A40205	Na+/H+-exchanging
24	85	7.3	605	A36361	glucose transport
25	84	7.2	463	AB0807	phosphoglycerate t
26	83.5	7.1	912	T49399	hypothetical prote
27	83	7.1	157	G02355	tumor-associated m
28	83	7.1	375	A64183	xylose transport p
29	83	7.1	395	S73531	CDP-diglyceride sy

ALIGNMENTS

RESULT 1

A39484

androgen-withdrawn apoptosis protein RVPI, prostatic - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000

C:Accession: A39484

R:Briehl, M.M.; Miesfeld, R.L.

Mol. Endocrinol. 5, 1381-1388, 1991

A:Title: Isolation and characterization of transcripts induced by androgen withdrawal an

A:Reference number: A39484; MUID:92130987; PMID:1723140

A:Accession: A39484

A:Molecule type: mRNA

A:Residues: 1-280 <BSI>

A:Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858

C:Genetics: RVP.1

A:Gene: RVP.1

C:Superfamily: rat androgen-withdrawn apoptosis protein RVP1

Query Match 41.7%; Score 489; DB 2; Length 280;

Best Local Similarity 42.6%; Pred. No. 2e-39;

Matches 100; Conservative 41; Mismatches 72; Indels 22; Gaps 4;

Qy	5	ALEIAGLFLGGVGMVGTVAVTVMPOVRVSAPFNIIVVEFWEGLMNCVROANIRMQC	64
Db	4	SLEITGSLAVLGLWLTIVCCALPMKRVSAFICSSITAIQTWEGLMNCV-QSTGMQCC	62
Qy	65	KYVDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILLTAGI	124
Db	63	KMYDSLIALPQDLQARALIVSILLAAFGLLVALVGAQCTNCVQD-ETAKAKITIVAGV	121
Qy	125	IFITITGMVVLIPVSWANAIIRDYFNSVNAQKRELGEALYLGWTTALVILVGGALFCC	184
Db	122	LFLLAAVLTILVPSWSANTIIRDYFNPFLVPEAQKREMGTLGYVGWAAALQLLGGALLCC	181
Qy	185	VFCNEKSSSYR--YSIP-----SHRTTQKSYHTGKSPSVY	219
Db	182	SCPPEKYAPTILKLYSAPRSTGCTGTAYDRKTTTSRPGARTPHHHYQPSMY	236

RESULT 2

A44432

amino acid transport protein - pig

N:Alternate names: Na+/amino acid cotransporter, SAAT1

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999

C:Accession: A44432

R:Kong, C.T.; Yet, S.F.; Lever, J.E.

J. Biol. Chem. 268, 1509-1512, 1993

A:Title: Cloning and expression of a mammalian Na+/amino acid cotransporter with sequenc

A:Reference number: A44432; MUID:93131881; PMID:8420925

A:Accession: A44432

A:Molecule type: nucleic acid

A;Residues: 1-660 <KON>
A;Cross-references: GB:L02900; NID:g164666; PIDN:AAC37325.1; PID:g164667
A;Experimental source: kidney epithelial cell line LLC-PK1
A;Note: sequence extracted from NCBI backbone (NCBIP:122778)
C;Superfamily: proline carrier protein
C;Keywords: amino acid transport; membrane protein

Query Match 8.6%; Score 100.5; DB 2; Length 660;
Best Local Similarity 27.0%; Pred. No. 0.11; Mismatches 25; Gaps 6;
Matches 38; Conservative 23;

QY 54 CVRQANIRMOCKIYD-SLLALSPDLQAARGLMCAASVMSFLAFMAILGMKTRCTG-- 110
DQ 351 CVKHCGETVGCNSYAYPLVLMELPGLGLMLSVMLASLMSLSIFNSASTLFTMDLY 410
QY 111 ---NEKVAHILLTAGIIFIITGMVVLIPVSVWANAIRDFYNSIVNVAQKRELGEAL-- 165
DQ 411 TKIRQAQSEKELLIAAGRLFII--LLIVISIVW-----PLVQAQNGQLPHYTES 458
QY 166 ---YLGWTTALVLIYGGALFC 183
DQ 459 ISSYLGPPIAAVFLM--ALFC 477

RESULT 3
A49182
Integral membrane protein MP20 - rat
N;Alternate names: lens membrane protein MP20
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A49182; S27883
R;Kumar, N.M.; Jarvis, L.J.; Tenbroek, E.; Louis, C.F.
Exp. Eye Res. 56, 35-43, 1993
A;Title: Cloning and expression of a major rat lens membrane protein, MP20.
A;Reference number: A49182; MUID:93162128; PMID:7679355
A;Accession: A49182
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-173 <KUM>
A;Cross-references: GB:S55224; NID:g265405; PIDN:AAB25334.1; PID:g265406
A;Experimental source: lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124760, NCBIP:124761)
R;Kumar, N.M.; Jarvis, L.J.; Tenbroek, E.; Louis, C.F.
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and expression of a major lens membrane protein, MP20.
A;Reference number: S27883
A;Accession: S27883
A;Molecule type: mRNA
A;Residues: 1-173 <KUM2>
A;Cross-references: EMBL:M87053; NID:g205514; PIDN:AAA41631.1; PID:g205515
C;Superfamily: growth arrest-specific protein
C;Keywords: membrane protein

Query Match 8.5%; Score 99.5; DB 2; Length 173;
Best Local Similarity 21.9%; Pred. No. 0.035;
Matches 43; Conservative 25; Mismatches 75; Indels 53; Gaps 9;

QY 10 GLFLGGVGMVGTVAIVTVPQW---RVSAFTIENNVFENFEGGLWNCVQANIRMOCKI 66
DQ 8 GLFCAWVGTLLVVATADTHWQVRUGSGFAH-----QGLWRYCLGN-----KCFL 53
QY 67 YDSILALSPDLQAARGLM---CAAS--VNSFLAFMAILGMKTRCTGDNKVKAHIL 119
DQ 54 QTESIAY--WNATRAFMILSALCATSGILINGVLAFAQQSTFTLSR-----p 98
QY 120 LTAGIIFIITGMVVLIPVSVWANAIRDFYNSIVNVAQKRELGE-----ALYLGWTTALV 174
DQ 99 FSAGIMFFASTLFLVLLALA-----IYTGVTVSFLGRFGDWRFWSYILGWVALLM 149
QY 175 LIVGGALFCCVFCNCE 190
DQ 150 TFFAGIFYMCAIRMHE 165

RESULT 4
S10196
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chicken mitochondrion
C;Species: mitochondrion Gallus gallus (chicken)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Jun-2002
C;Accession: S10196
R;Desjardins, P.; Morais, R.
J. Mol. Biol. 212, 599-634, 1990
A;Title: Sequence and gene organization of the chicken mitochondrial genome. A novel gen
A;Reference number: S10187; MUID:90230301; PMID:2329578
A;Accession: S10196
A;Molecule type: DNA
A;Residues: 1-459 <DES>
A;Cross-references: EMBL:X52392; NID:g12960; PIDN:CAA36634.1; PID:g12970
C;Genetics:
C;Gene: ND4
A;Genome: mitochondrion
A;Genetic code: NDC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 8.3%; Score 97.5; DB 2; Length 459;
Best Local Similarity 23.7%; Pred. No. 0.15;
Matches 51; Conservative 45; Mismatches 86; Indels 33; Gaps 12;

QY 11 LFLGGVGMVGTVAIVTVPQWVRVSFTIENNVFENFEGGLWNCVQANIRMOCKIYD 68
DQ 236 LXLGGVGI---MRVTLMB-PVSNFLHYPLTLA-LWGALMTSSICLRDTLK----- 283
QY 69 SLLALSPDLQAARGLMCAASVM-----SFLAFMAILGMKCTR---CTGDNEKVAH--- 117
DQ 284 SLIAYSS--VSHMGLVIAASMIQTQWSFGAMILMHSGLTSSLLFCLANTYVERHSRI 341
QY 118 ILLTAGIIFIITGMVVLIPVSVWANAIRDFYNSIVNVAQKRELGAALYLGWTTALVLI 177
DQ 342 LILTRG----LQELLPLMSVWMLLANLTNMLPPTTNMAELTIMVALF-NWSSPTILT 396
QY 178 GGA-LFCCVFCNCEKSSSYRYSIPSHRTQKSYHT 211
DQ 397 GTATLLTASVTLVMLLTQGTLPSPHITTPNSNT 431

RESULT 5
A48300
lens membrane protein MP19 - bovine
N;Alternate names: lens fiber cell membrane protein MP18; lens fiber membrane intrinsic
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A48300; A34490; S05010
R;Gutekunst, K.A.; Rao, G.N.; Church, R.L.
Curr. Eye Res. 9, 955-961, 1990
A;Title: Molecular cloning and complete nucleotide sequence of the cDNA encoding a bovin
A;Reference number: A48300; MUID:91114349; PMID:2276272
A;Accession: A48300
A;Molecule type: mRNA
A;Residues: 1-173 <GUT>
A;Cross-references: GB:L04188; NID:g163294; PIDN:AAA30621.1; PID:g163295
R;Louis, C.F.; Hur, K.C.; Galvan, A.C.; Tenbroek, E.M.; Jarvis, L.J.; Eccleston, E.D.; J
J. Biol. Chem. 264, 19967-19973, 1989
A;Title: Identification of an 18,000-Dalton protein in mammalian lens fiber cell membra
A;Reference number: A34490; MUID:90062105; PMID:2584203
A;Accession: A34490
A;Molecule type: protein
A;Residues: 1-23 <LOU>
A;Experimental source: lens
R;Rao, G.N.; Gutekunst, K.A.; Church, R.L.
FEBS Lett. 250, 483-486, 1989
A;Title: Bovine lens 23, 21 and 19 kDa intrinsic membrane proteins have an identical am
A;Reference number: S05010; MUID:89325619; PMID:2473922
A;Accession: S05010
A;Molecule type: protein
A;Residues: 1-20 <RAO>

C;Superfamily: growth arrest-specific protein
C;Keywords: membrane protein
F;1-173/Product: lens membrane protein MP19 #status predicted <MAT>

Query Match 8.1%; Score 95.5; DB 2; Length 173;
Best Local Similarity 21.4%; Pred. No. 0.084; 76; Indels 53; Gaps 9;
Matches 42; Conservative 25; Mismatches 25

QY 10 GLFLGGVGMVGTAVTVMPOW---RVSAFIENNIIVVFENFWEGLWMNCVROANIRMOCKI 66
DB 8 GLFCWVGTILLVWATATDHMQYRLSGAPAH-----QGLWRYC-----LGTKCYL 53

QY 67 YDSLALSPDLQAAGLM-----CAAS--VMSFLAFMAILGMKCTRCTGDNKVKAHIL 119
DB 54 QTESIAY---WNATRAFMLSSLCATSGIIMGIWAFQAQPTFTLRL-----P 98

QY 120 LTAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGE-----ALYLGWTTALV 174
DB 99 PSAGIMPEASTFFVLLALA-----IYGTIVSFILGRFRGDMRFSWVILGWALLM 149

QY 175 LIVGGLFCCVFCNCE 190
DB 150 TFFAGIFMCAYRMHE 165

RESULT 6
Tl1489
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - rabbit mitochondrion (fragment)
C;Species: mitochondrion Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: Tl1489
R;Glissi, C.; Gullberg, A.; Arnason, U.
Genomics 50, 161-169, 1998
A;Title: The complete mitochondrial DNA sequence of the rabbit, Oryctolagus cuniculus.
A;Reference number: 217275; MUID:98317530; PMID:9653643
A;Accession: Tl1489
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-459 <GIS>
A;Cross-references: EMBL:AJ001588; NID:g3293006; PIDN:CAA04856.1; PID:g3293016
C;Genetics:
A;Gene: NADH4
A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 8.1%; Score 94.5; DB 2; Length 459;
Best Local Similarity 20.8%; Pred. No. 0.29;
Matches 48; Conservative 41; Mismatches 81; Indels 61; Gaps 12;

QY 11 LFLGGVGMVG-TVAVTVMPOWRVSAFIENNIIVVFENFWEGLWMN---CVRQANIR----- 61
DB 236 LKLGYGMRITILLSPITDMAYPFL-----MLSLW-GNMTSSICLTQTLKSLIAY 288

QY 62 -----MCKYDYSLLALSPDLQAAGLMCAASVMSFLAFMAILGMKCTRCTGDNKVK 116
DB 289 SSVSHMALVIVAILIQPFWSFGATALMTAHLGTSLLFCLA-----NSNVERIHS 339

QY 117 HIILTAGIIFIITGMVVLIPVS---WYANAIIRDFYNSIVNVAQKRELGEALYL-----GW 169
DB 340 RTWLLA-----RLQILFLMAAWVIVASLTNLALPPTINL-----LGELLIIMASFSW 388

QY 170 TTLVLIVGGLFCCVFCNCEKSSSYRISPSHRTTOK---SYHTGKKSPS 217
DB 389 SNLTILMGNTLITAL-----YSLYMLSTTGQKFTHTNNISPT 429

RESULT 7
T33784
hypothetical protein Y39D8A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000

C;Accession: T33784
R;Becker, M.; Graves, T.; Yoakum, M.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid Y39D8A.
A;Reference number: Z21409
A;Accession: T33784
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-468 <BEC>
A;Cross-references: EMBL:AF101314; PIDN:AAC69224.1; GSPDB:GN00023; CESP:Y39D8A.1
A;Experimental source: strain Bristol N2; clone Y39D8A
C;Genetics:
A;Gene: CESP:Y39D8A.1
A;Map position: 5
A;Introns: 55/2; 118/1; 150/2; 239/1; 302/1; 359/2; 404/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y39D8A.1

Query Match 8.0%; Score 94; DB 2; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.33;
Matches 59; Conservative 31; Mismatches 84; Indels 70; Gaps 11;

QY 6 LEIAGLF--LGGVGMVGTAVTVMPOWRVSAFIENNIIVVFENFWEGLWMNC----- 54
DB 192 LEINLFSATGTSVLGIITFFVMPKSDVENCIESSEKKBTFLEALKLCTSLVSPTML 251

QY 55 -----VROANIRMOCKIYDLSILALSPDLQAAGLMCA-----SVMSFL 93
DB 252 QLFLFLVLSGFNTSFWLSVPT--AMSFQWQNSKLIYLAAYVSLGVSGEVIIGLAI 309

QY 94 AFMAILGMKCTRCTGDNKVKAHILTAGIIFIITGMVVLIPVSWANAIIRDFYNSIV 153
DB 310 SKRIKDFGQKPT-----MTIGAIF-ITWYCAMIHMSTPYDAPIRPTSK--- 351

QY 154 NVAQKRELGEALYLGTWLTALVILVGGALFCCV-FCC--NEKSSSYRISPSHRTTQ 206
DB 352 -----BPLFFGHSHYLLALIIG--LFCIGGCCVNSRVITCALLMPKRRPQAFSVS 400

QY 207 KSYH 210
DB 401 KIYH 404

RESULT 8
C75609
amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75609
R;White, O.; Eise, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-484 <WHI>
A;Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12224.1; PID:g646051
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0136
A;Map position: 2

Query Match 7.9%; Score 93; DB 2; Length 484;
Best Local Similarity 26.4%; Pred. No. 0.42;
Matches 28; Conservative 17; Mismatches 45; Indels 16; Gaps 3;

QY 6 LEIAGLFLGG-----VGMVGTAVTVMPOWRVSAFIENNIIVVFENFWEGLWMN 53
DB 144 LSTADLYIGGFAYSVWRVWRPAGVAGAFAPVPLLGKWNLTGLVQEVNRNADTFWPQLGTH 203

QY 54 CVRQANIRMOCKIYDLSILALSPDLQAAGLMCAASVMSFLAFWMAI 99

```

Db      204  ---AALSVALIIAALLGLPLGIAAARTRLAGGVLGFASFLQTI 245
      | : : : : | | | | : | | | | : | : | : |
RESULT 9
S48921
hypothetical protein YHL047c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
C:Accession: S48921
R:Favelllo, T.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of S. cerevisiae cosmid 9196.
A:Reference number: S46794
A:Accession: S48921
A:Molecule type: DNA
A:Residues: 1-637 <FAV>
A:Cross-references: EMBL:U11583; NID:g2289854; PID:AA65059.1; PID:g2289876; GSPDB:GN00
C:Genetics:
A:Gene: SGD:TAF1; MIPS:YHL047C
A:Cross-references: SGD:S0001039
A:Map position: 8L
C:Superfamily: conserved probable membrane protein YCL073C

```

Query March	7.9%;	Score 92.5;	DB 2;	Length 637;	
Best Local Similarity	21.6%;	Pred. No. 0.63;			
Matches 52;	Conservative 43;	Mismatches 63;	Indels 83;	Gaps 15;	
Qy	6	LEIAG--LFLGGVGWV---GTVAVTVMPOQRVSAFIENNIIVFE-----NFWE-----	48		
Db	284	LDVVGVLLFTAGVGCILVPLTLAGGVSTNNFNSKIIGFPVLGFLVLPFGFIYWSERLALVP	343		
Qy	49	-----GLWNCVROANIRMQ---CKIYD-----SLIALSPLOAARGLMCAAS	88		
Db	344	FAPFKLLKDRGVW-----APLGIMFFICFYQMAAGVLYTILVAVDESAS-----SATR	393		
Qy	89	VMSFLAFNMAL-----LGMKCTRCTGDNEKVKAHIL-----LTAGIIF-----	126		
Db	394	IINLYSFVAVVAPPLGLIVTR---SSRLKSYIIFGGSLYFIITMGLFYRRSQDADGG	449		
Qy	127	IITGMVVLIPVSWANAIIRDFFYN--STVNVAQXRELGALYIGMTTALVLIVGGLFCC	184		
Db	450	IIAGVLI-----WGLSSCLFDPIIVSLIQSVTSHENMATVIALNYT---VFRIGSAVAA	501		
Qy	185	V	185		
Db	502	I	502		

RESULT 10
B40204
Na+/H+-exchanging protein 3 - rat
N/Alternate names: Na+/H+ antiporter
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C/Accession: B40204
R:Orlowski, J.; Kandasamy, R.A.; Shull, G.E.
J. Biol. Chem. 267, 9331-9339, 1992
A/Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDNA
xally related proteins.
A/Reference number: A40204; MUID: 92250539; PMID: 1577762
A/Accession: B40204
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-831 <ORF>
A/Cross-references: GB: M85300; NID: G205706; PIDN: AAA41702.1; PID: g205707
C/Keywords: transmembrane protein

Query Match 7.9%; Score 92.5; DB 2; Length 831;
Best Local Similarity 19.9%; Pred. No. 0.82;
Matches 49; Conservative 43; Mismatches 69; Indels 85; Gaps 12;
OV 2 ATHALEIAGLFLGG-----VGMV-----GTVAVTMPQWRVSATIE---NNIVVFENFW 47

[illegible]

RESULT 11

S37078
chloride channel protein CLC-1 - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: S37078; S36602; I38014; S36743
R:Steinmeyer, K.; Lorenz, C.; Pusch, M.; Koch, M.C.; Jentsch, T.J.
submitted to the EMBL Data Library, September 1993
A:Description: Multimeric structure of CLC-1 chloride channel revealed by muta
A:Reference number: S37078
A:Accession: S37078
A:Molecule type: mRNA
A:Residues: 1-988 <STB1>
A:Cross-references: EMBL:Z25884; NID:G398160; PID:G398161
R:Steinmeyer, K.; Lorenz, C.; Pusch, M.; Koch, M.C.; Jentsch, T.J.
submitted to the EMBL Data Library, August 1993
A:Description: Multimeric structure of CLC-1 chloride channel revealed by muta
A:Reference number: S36602
A:Accession: S36602
A:Molecule type: DNA
A:Residues: 1-988 <STB2>
A:Cross-references: EMBL:Z25587; NID:G397142; PID:G397143
R:Lorenz, C.; Meyer-Kleine, C.; Steinmeyer, K.; Koch, M.C.; Jentsch, T.J.
Hum. Mol. Genet. 3, 941-946, 1994
A:Title: Genomic organization of the human muscle chloride channel CLC-1 and
A:Reference number: I38014; MUID:95038751; PMID:7951242
A:Accession: I38014
A:Status: preliminary; translated from GB/EMBL/DDBB

A:Residues: 1-7 <RES>
A:Cross-references: EMBL:Z31372; NID:G479168; PIDN:CAA83243.1; PID:G580290
R:Koch, M.C.; Steinmeyer, K.; Lorenz, C.; Ricker, K.; Wolf, F.; Otto, M.; Zolli-
Science 257, 797-800, 1992
A:Title: The skeletal muscle chloride channel in dominant and recessive human
A:Reference number: S36743; MUID:92358240; PMID:1379744
A:Accession: S36743
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 171-988 <KOC>
A:Cross-references: EMBL:M97820
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August
C:Genetics:
A:Gene: GDB:CLCN1
A:Cross-references: GDB:134688; OMIM:118425
A:Map position: 7q32-qter
C:Superfamily: CBS homology
C:Keywords: transmembrane protein
F:612-662/Domain: CBS homology <CBS>

Query Match	7.8%	Score 91.5;	DB 2;	Length 988;
Best Local Similarity	22.2%;	Pred. No.1.2;		
Matches 50;	Conservative	32;	Mismatches 72;	Indels 71;
				Gaps 1

QY 1 MATHALEIAGL-----FLGGVGMVGTAVTVMPOWRVSFIENN----- 39
Db 386 LAKHRLLYGIVTFVIASTFFPPGMQFAGMELPREAISTFLDNNNTWKVHAGDPESLQG 445
QY 40 -----IVVFENFEGLMNCVRQANRMOC-----KIYDSLAA- 72
Db 446 SAVWIHPRVNVVILIFLFFVMEKFWMSIV-ATTMPICGGFMPPVVLGAAGRLVGEIMAM 504
QY 73 LSPDLOAAGLMCAASVMSFLAFMMAILGMKCTCTGDNEKVAHILLTAGIIFIITG-- 130
Db 505 LFPD-----GILFDDLIYKILPGGVAIG--AAALTG---AVSHTVSTAVICFELTGOI 553
QY 131 -----MVLIPVSVANAIIRDYFNSIVNVAQKRELGEALYLGW 169
Db 554 AHILPMWAVILANWVAOSLQSLYDSIQVKLPLYLPD---LGW 595
RESULT 12
AH0781
probable membrane protein STY2426 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0781
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0781
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02574.1; PID:gl6503432; GSPDB:GN00176
C:Genetics:
A:Gene: STY2426
Query Match 7.6%; Score 89.5; DB 2; Length 380;
Best Local Similarity 20.3%; Pred. No. 0.71;
Matches 50; Conservative 41; Mismatches 82; Indels 73; Gaps 12;
QY 12 FLGGVGMVGTAVTVM-----PQWRVSFIENNIVVFENFEGLMNCVRQANI 60
Db 9 FVRGVALIGILLNISAFGLPKAAAYLNPW-----YGAIVPEDAWSWAILDIVAQAKF 61
QY 61 RMQCKIYDSLIALSPDLOAARG---LMCAASVMSFLAFMMA-----ILGMKC 104
Db 62 ---LTLFALLFAGLQMLPRGKOWIOSRLTLLVLLGFHALFWDDGIDLLAYGLVGLIC 118
QY 105 TRCTGDNEKVAHILLTAGIIFIITGMVVLIPV-----SWV--ANAIIRDYF--- 149
Db 119 WRLVRDAPSVKS--LFTNTGILLYLVGIGVLLGLVSVSSSETSRATPDASAILYKWKWL 176
QY 150 ----NSIVNVAQKRE---LGEALYLGWTTALVILVGGALPCCVCCNEKSSSY---RYSI 199
Db 177 NGGMEATSNRAEMLNSLLALGAQYQWQLAGMILLGAALM-----RSGMLKGQYSL 227
QY 200 PSHRTT 205
Db 228 RHYERT 233
RESULT 13
T11358
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Daphnia pulex mitochondrion
C:Species: mitochondrion Daphnia pulex
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11358
R:Crease, T.J.
Gene 233, 89-99, 1999
A:Title: The complete sequence of the mitochondrial genome of Daphnia pulex (Cladocera:

A:Reference number: Z17264; MUID:99307147; PMID:10375625
A:Accession: T11358
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-440 <CRE>
A:Cross-references: EMBL:AF117817; NID:g4927669; PID:g4927678; PIDN:AAD33238.1
C:Genetics:
A:Gene: ND4
A:Genome: mitochondrion
A:Genetic code: SGC4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 7.6%; Score 89; DB 2; Length 440;
Best Local Similarity 23.7%; Pred. No. 0.93;
Matches 51; Conservative 29; Mismatches 51; Indels 84; Gaps 13;
QY 8 TAG--LFLGGVGMVGTAVTVMPOWRVSFIENNIVVFENFEGLMW-----NCVRQ 57
Db 215 LAGVLLKLGGMV-----RVVPYIELSLSEFSSFLMSVSLVGGVTASVICIRQ 263
QY 58 ANIRMOCK---IYDS-----LLALSPDLOAARGL-----MCAASVMSFLAFMMA 98
Db 264 TD-----CKSLVAYSSVAHMAVLVLLGWINSVGLAGVVTIMISHGLGCSGLFSLVGMIE 319
QY 99 ILGMKCTCTGDNEKVAHILLTAGIIFIITGMVVLIPVS---WVANAIIRDYFNSIVNV 155
Db 320 RMGTRS-----IILRSLLTAPLSTLWM-----FLFAISNM 351
QY 156 A---QKRELGPALYL-----GWTTLVLIVGGALF 182
Db 352 AAPSPNLLGE-IYLFITSSIGWGGSSLLVGGLSF 385
RESULT 14
S33044
hypothetical protein - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S33044
R:Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A:Reference number: S32973
A:Accession: S33044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-618 <FAR>
A:Cross-references: EMBL:V01555
Query Match 7.5%; Score 88; DB 2; Length 618;
Best Local Similarity 26.1%; Pred. No. 1.6;
Matches 37; Conservative 15; Mismatches 66; Indels 24; Gaps 4;
QY 61 RMQCKIYDSLIALSPDLOAARGLMCAASVMSFL-----AFMMAILGM-----KCTRCT 108
Db 2 RAOCFALLSATCLITNLSSAASSSSAASRVGFLGTCKNSAKLAHLNQVTRTPPCPPFS 61
QY 109 GDNEKVAHILLTAGIIFIITGMVVLIPVSWANAIIRDYF--YNSIVNVAQKRELGEALYL 167
Db 62 GREARLKPFHFFSWSTFM-----LSWPNNAITLREIRTRAATNLTHHPLHVDLYH 110
QY 168 GWTTALVILVGGALFCCVCCN 189
Db 111 ASPQTPFLTRSGALYRFVTCN 132
RESULT 15
T23909
hypothetical protein R04Fl1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jun-2003
C:Accession: T23909
R:Harris, B.

submitted to the EMBL Data Library, June 1996
A:Reference number: Z19816
A:Accession: T23909
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-297 <WIL>
A:Cross-references: EMBL:Z74475; PIDN:CAA98959.1; GSPDB:GN00023; CESP:R04F11.1
A:Experimental source: clone R04F11
C:Genetics:
A:Gene: CESP:R04F11.1
A:Map position: 5
A:Introns: 44/3; 82/3; 120/1; 156/1; 244/3
C:Superfamily: uncharacterized conserved protein K10D6.2b

Query Match 7.4%; Score 87; DB 2; Length 297;
Best Local Similarity 21.7%; Pred. No. 0.96; Mismatches 83; Indels 80; Gaps 13;
Matches 55; Conservative 36;

QY	6	LEIAGLFLGGVGMVGTAVTVMFPQWRVSAPFIENNIIVVFENFWEGLMNCV-----	55
Db	57	LLVTSIFLIVSGLLITAFSLFSEPLWEVDVDFPRSHL-----SHHGLWWDCTIVHHETLIPLH	112
QY	56	-RQANIR-----MCKIYDSL-LALSPDLQAARGIMCAA-----SYMSFLAF	95
Db	113	EDQAEIRGDRCDKMDSSVQASLRVALEKGEARELLLRFLPHKGVIFFAVTFVFG	172
QY	96	MMAILGMKTRCTGDNKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRDFYNS----	151
Db	173	LISILIGSCSPCFPPNA-----LLYVVGW--FMTGACSL-----ADIIYIFAFNOKPIF	220
QY	152	-----IVNVACKRE-----LGEALYLGWTTALVLIYG--GALFCCVF-----	186
Db	221	TKEQSEPHQEVLSRRREGSGIPYKRLGIATYMEFGSMLLIAAFIESIFCAVFLITSKH	280
QY	187	-----CCNEKSSSYR	196
Db	281	AHDVCCTSR--KEYR	293

Search completed: September 1, 2004, 16:56:26
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:54:39 ; Search time 49 Seconds
(without alignments)
1444.651 Million cell updates/sec

Title: US-10-063-732-120

Perfect score: 1172

Sequence: 1 MATHALEIAGLFLGGVGMWG.....QKSHYTKKSPSVRSQYV 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	225	9	US-09-731-872-405
2	1172	100.0	225	10	US-09-946-374-328
3	1172	100.0	225	10	US-09-876-997-405
4	1172	100.0	225	12	US-10-206-915-358
5	1172	100.0	225	12	US-10-199-670-358
6	1172	100.0	225	12	US-10-201-858-358
7	1172	100.0	225	12	US-10-205-890-358
8	1172	100.0	225	12	US-10-208-024-358
9	1172	100.0	225	12	US-10-201-853-358
10	1172	100.0	225	12	US-10-063-745-120
11	1172	100.0	225	12	US-10-063-513-120
12	1172	100.0	225	12	US-10-063-513-120
13	1172	100.0	225	12	US-10-063-515-120
14	1172	100.0	225	12	US-10-063-549-120
15	1172	100.0	225	12	US-10-063-569-120

16	1172	100.0	225	12	US-10-063-551-120	Sequence 120, App
17	1172	100.0	225	12	US-10-174-581-358	Sequence 358, App
18	1172	100.0	225	12	US-10-176-483-358	Sequence 358, App
19	1172	100.0	225	12	US-10-176-749-358	Sequence 358, App
20	1172	100.0	225	12	US-10-176-914-358	Sequence 358, App
21	1172	100.0	225	12	US-10-176-915-358	Sequence 358, App
22	1172	100.0	225	12	US-10-006-485A-328	Sequence 328, App
23	1172	100.0	225	12	US-10-013-907A-328	Sequence 328, App
24	1172	100.0	225	12	US-10-015-499A-328	Sequence 328, App
25	1172	100.0	225	12	US-10-063-555-120	Sequence 120, App
26	1172	100.0	225	12	US-10-063-563-120	Sequence 120, App
27	1172	100.0	225	12	US-10-063-594-120	Sequence 120, App
28	1172	100.0	225	12	US-10-063-553-120	Sequence 120, App
29	1172	100.0	225	12	US-10-063-554-120	Sequence 120, App
30	1172	100.0	225	12	US-10-176-484-358	Sequence 358, App
31	1172	100.0	225	12	US-10-180-550-358	Sequence 358, App
32	1172	100.0	225	12	US-10-183-014-358	Sequence 358, App
33	1172	100.0	225	12	US-10-187-738-358	Sequence 358, App
34	1172	100.0	225	12	US-10-187-740-358	Sequence 358, App
35	1172	100.0	225	12	US-10-187-883-358	Sequence 358, App
36	1172	100.0	225	12	US-10-194-363-358	Sequence 358, App
37	1172	100.0	225	12	US-10-194-460-358	Sequence 358, App
38	1172	100.0	225	12	US-10-194-463-358	Sequence 358, App
39	1172	100.0	225	12	US-10-194-484-358	Sequence 358, App
40	1172	100.0	225	12	US-10-195-884-358	Sequence 358, App
41	1172	100.0	225	12	US-10-195-896-358	Sequence 358, App
42	1172	100.0	225	12	US-10-196-744-358	Sequence 358, App
43	1172	100.0	225	12	US-10-196-755-358	Sequence 358, App
44	1172	100.0	225	12	US-10-197-704-358	Sequence 358, App
45	1172	100.0	225	12	US-10-197-704-358	Sequence 358, App

ALIGNMENTS

RESULT 1
US-09-731-872-405
; Sequence 405, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 405
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-405

Query Match	100.0%;	Score 1172;	DB 9;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 4.9e-119;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MATHALEIAGLFLGGVGMWGTVAVTVPQWRVSFAFTENNIIVFENFWEGLMNCVROANI	60	
Db	1	MATHALEIAGLFLGGVGMWGTVAVTVPQWRVSFAFTENNIIVFENFWEGLMNCVROANI	60	
QY	61	RMCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGNEKVKAHILL	120	
Db	61	RMCKIYDLSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGNEKVKAHILL	120	
QY	121	TAGIIFIITGMVYLIPVSWVANAIIRDVNSIVNVAQKRELGEALVIGTWTALVIVGGA	180	

Db 121 TAGIIFLITGMVLIPVSWANAIIRDFFYNVIVNVAQKRELGEALYLGWTTALVIVGA 180
QY 161 LFCVFCCKEKSSSRYSTPSHRTTQKSYHTGKSPSVYRSQYV 225
Db 181 LFCVFCCKEKSSSRYSTPSHRTTQKSYHTGKSPSVYRSQYV 225

RESULT 2
US-09-946-374-328
; Sequence 328, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; TITLE OF INVENTION: Acids Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
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; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
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; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29

; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
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; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
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; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1172; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60

Qy 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

Db 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

Qy 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180

Qy 181 LFCCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 3
US-09-876-997-405
; Sequence 405, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 USA CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 405
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-997-405

Query Match 100.0%; Score 1172; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANI 60

Qy 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120

Qy 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180

Qy 181 LFCCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCCVFCNCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 4
US-10-206-915-358
; Sequence 358, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-358

Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOQWVSFAFIENNVVFENFWEGLMNCVROANI 60
Db 1 MATHALEIAGLFLGGVGMGTVAVTVMPOQWVSFAFIENNVVFENFWEGLMNCVROANI 60
QY 61 RMCKIYDLSLLASPDLOAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDLSLLASPDLOAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWANAIIRDFYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDFYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225
Db 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225

RESULT 7
US-10-205-890-358
; Sequence 358, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-358

Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMGTVAVTVMPOQWVSFAFIENNVVFENFWEGLMNCVROANI 60
Db 1 MATHALEIAGLFLGGVGMGTVAVTVMPOQWVSFAFIENNVVFENFWEGLMNCVROANI 60
QY 61 RMCKIYDLSLLASPDLOAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDLSLLASPDLOAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWANAIIRDFYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDFYNSIVNVAOKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225
Db 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225

RESULT 8
US-10-208-024-358
; Sequence 358, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266

Fri Sep 3 10:15:56 2004

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-358

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNVFENFEGLMWNCVRQANI 60
DB 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNVFENFEGLMWNCVRQANI 60

QY 61 RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
DB 61 RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120

QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
DB 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCCVFCCKEKKSSSYRSPSHRTTQKSYHTGKSPSVYRSQYV 225
DB 181 LFCCVFCCKEKKSSSYRSPSHRTTQKSYHTGKSPSVYRSQYV 225

RESULT 9
US-10-201-853-358
; Sequence 358, Application US/10201853
; Publication No. US20040053359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-358

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNVFENFEGLMWNCVRQANI 60
DB 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNVFENFEGLMWNCVRQANI 60

QY 61 RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
DB 61 RMQCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120

QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
DB 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180

QY 181 LFCCVFCCKEKKSSSYRSPSHRTTQKSYHTGKSPSVYRSQYV 225
DB 181 LFCCVFCCKEKKSSSYRSPSHRTTQKSYHTGKSPSVYRSQYV 225

RESULT 10
US-10-063-745-120
; Sequence 120, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION data removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-120

Query Match      100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNVFENFEGLMWNCVRQANI 60
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Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Qy 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Qy 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Qy 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225

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RESULT 11

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US-10-063-512-120
; Sequence 120, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-120

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Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Qy 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Qy 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Qy 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225

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RESULT 12

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US-10-063-513-120
; Sequence 120, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

```

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-120

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Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Qy 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFWMAILGKCTCTGDNKVKAHILL 120
Qy 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSVNAQKREIGALYLGWTTALVLI VGG 180
Qy 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSRYISPSHRTTQKSYHTGKSPSVYSRSQYV 225

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RESULT 13

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US-10-063-515-120
; Sequence 120, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-120

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Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFIENNIIVVFENFWEGLMNCVRQANI 60

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QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 14
US-10-063-549-120
; Sequence 120, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-549-120

Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 15
US-10-063-569-120
; Sequence 120, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-120
Query Match 100.0%; Score 1172; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSFAFIENNIIVFENFWEGLWMNCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
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Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:57:25; Search time 19 Seconds
(without alignments)
611.360 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
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Searched: 389414 seqs, 51625971 residues

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Minimum DB seq length: 0
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Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	45.8	113	4	US-09-621-976-5695
2	9	4.0	22	4	US-09-205-258-869
3	9	4.0	202	4	US-09-205-258-344
4	9	4.0	220	4	US-09-603-552-13
5	9	4.0	247	4	US-09-130-491-15
6	8	3.6	225	4	US-09-489-039A-13977
7	8	3.6	420	4	US-09-252-991A-22253
8	8	3.6	1218	4	US-09-589-567-2
9	7	3.1	18	3	US-08-940-095-226
10	7	3.1	18	3	US-08-940-093-226
11	7	3.1	18	3	US-08-940-096-226
12	7	3.1	18	3	US-09-465-719-226
13	7	3.1	18	4	US-09-453-605-226
14	7	3.1	18	4	US-09-453-838-226
15	7	3.1	18	4	US-08-940-136-226
16	7	3.1	18	4	US-09-205-258-870
17	7	3.1	18	4	US-09-453-841-226
18	7	3.1	18	4	US-09-453-833-226
19	7	3.1	18	4	US-09-453-826-226
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21	7	3.1	89	4	US-09-245-281-33
22	7	3.1	89	4	US-09-207-359B-33
23	7	3.1	89	4	US-09-340-620A-33
24	7	3.1	89	4	US-09-865-364-33
25	7	3.1	99	4	US-09-621-976-4220
26	7	3.1	123	1	US-08-398-613A-20
27	7	3.1	123	1	US-08-398-612A-20

28	7	3.1	123	1	US-08-398-611A-20	Sequence 20, Appl
29	7	3.1	123	2	US-08-491-334A-20	Sequence 20, Appl
30	7	3.1	123	3	US-09-027-449-17	Sequence 17, Appl
31	7	3.1	123	3	US-08-804-444A-17	Sequence 17, Appl
32	7	3.1	123	3	US-09-026-985-17	Sequence 17, Appl
33	7	3.1	123	4	US-09-121-952A-17	Sequence 17, Appl
34	7	3.1	123	4	US-09-234-340A-17	Sequence 17, Appl
35	7	3.1	137	3	US-09-188-930-174	Sequence 174, Appl
36	7	3.1	137	4	US-09-312-283C-174	Sequence 174, Appl
37	7	3.1	185	4	US-09-198-452A-184	Sequence 184, Appl
38	7	3.1	225	4	US-09-673-395A-354	Sequence 354, Appl
39	7	3.1	230	4	US-09-663-600A-92	Sequence 92, Appl
40	7	3.1	230	4	US-09-663-600A-186	Sequence 186, Appl
41	7	3.1	237	1	US-08-398-612A-28	Sequence 28, Appl
42	7	3.1	237	1	US-08-398-611A-28	Sequence 28, Appl
43	7	3.1	237	2	US-08-491-334A-28	Sequence 28, Appl
44	7	3.1	237	3	US-09-027-449-25	Sequence 25, Appl
45	7	3.1	237	3	US-08-804-444A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-5695
; Sequence 5695, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5695
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -79...-1
; NAME/KEY: UNSURE
; LOCATION: 25
; OTHER INFORMATION: Xaa = *, Ser
US-09-621-976-5695

Query Match 45.8%; Score 103; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1e-91;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGFLGGVGMVGTVAVTVMPQWRVSFAIENNVVFENFWEGLMNCVROANI 60
Db 1 MATHALEIAGFLGGVGMVGTVAVTVMPQWRVSFAIENNVVFENFWEGLMNCVROANI 60
QY 61 RMCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMAILGMK 103
Db 61 RMCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMAILGMK 103

RESULT 2
US-09-205-258-869
; Sequence 869, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 869
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-869
Query Match 4.0%; Score 9; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 47 WEGLMNCV 55
DB 10 WEGLMNCV 18
RESULT 3
US-09-205-258-344
Sequence 344, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 344
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (202)
OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-344

Query Match 4.0%; Score 9; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMWNCV 55
Db 39 WEGLMWNCV 47
|||||

RESULT 4
US-09-603-552-13
Sequence 13, Application US/09603552
Patent No. 6590089
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
FILE REFERENCE: PC-0016 US
CURRENT APPLICATION NUMBER: US/09/603,552
CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 13
SOFTWARE: PERL Program
SEQ ID NO 13
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank No. 6590089 g2570129
US-09-603-552-13

Query Match 4.0%; Score 9; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMWNCV 55
Db 46 WEGLMWNCV 54
|||||

RESULT 5
US-09-130-491-15
Sequence 15, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-130-491-15

Query Match 4.0%; Score 9; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMWNCV 55
Db 46 WEGLMWNCV 54
|||||

RESULT 6
US-09-489-039A-13977
Sequence 13977, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13977
LENGTH: 225
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13977

Query Match 3.6%; Score 8; DB 4; Length 225;

Fri Sep 3 10:15:54 2004

us-10-063-732-120.olg6.rai

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; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; US-08-940-095-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 RELGEAL 165
Db 7 RELGEAL 13

RESULT 10
US-08-940-093-226
; Sequence 226 Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

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; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; US-08-940-095-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 RELGEAL 165
Db 7 RELGEAL 13

RESULT 10
US-08-940-093-226
; Sequence 226 Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

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/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/940,093
/ FILING DATE: 29-SEP-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0006-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 226:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6037323e
US-08-940-093-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
DB 7 RELGEAL 13

RESULT 11
US-08-940-096-226
/ Sequence 226, Application US/08940096
/ Patent No. 6046166
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/940,096
/ FILING DATE: 29-SEP-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
DB 7 RELGEAL 13

RESULT 12
US-09-465-719-226
/ Sequence 226, Application US/09465719
/ Patent No. 6265377
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/465,719
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,093
/ FILING DATE: 29-SEP-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0006-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 226:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6265377e
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US-09-465-719-226

Query Match 3.1%; Score 7; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
| | | | |
Db 7 RELGEAL 13

RESULT 13

US-09-453-605-226

Sequence 226, Application US/09453605

Patent No. 6329341

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453-605

FILING DATE: 26-No. 6329341-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,095

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 226:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6329341e

SEQUENCE DESCRIPTION: SEQ ID NO: 226:

US-09-453-605-226

Query Match 3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
| | | | |
Db 7 RELGEAL 13

RESULT 14

US-09-453-838-226

Sequence 226, Application US/09453838
Patent No. 6376464
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6376464e
US-09-453-838-226

Query Match 3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 RELGEAL 165
| | | | |
Db 7 RELGEAL 13

RESULT 15

US-08-940-136-226

Sequence 226, Application US/08940136

Patent No. 6518412

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: GENE THERAPY APPROACHES TO

SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0007-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6518412e
US-08-940-136-226

Query Match 3.1%; Score 7; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 159 RELGEAL 165
Db 7 RELGEAL 13

Search completed: September 1, 2004, 17:00:12
Job time : 21 secs

11/11/11

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:58:25 ; Search time 49 Seconds
(without alignments)
1444.651 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFLGGVMVG.....QKSHYTKKSPVRSQVY 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1297172 seqs, 314612898 residues

Word size : 6
Total number of hits satisfying chosen parameters: 5827

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	100.0	225	9	US-09-731-872-405
2	225	100.0	225	10	US-09-946-374-328
3	225	100.0	225	10	US-09-876-997-405
4	225	100.0	225	12	US-10-206-915-358
5	225	100.0	225	12	US-10-199-670-358
6	225	100.0	225	12	US-10-201-858-358
7	225	100.0	225	12	US-10-205-890-358
8	225	100.0	225	12	US-10-208-024-358
9	225	100.0	225	12	US-10-201-853-358
10	225	100.0	225	12	US-10-063-745-120
11	225	100.0	225	12	US-10-063-512-120
12	225	100.0	225	12	US-10-063-513-120
13	225	100.0	225	12	US-10-063-515-120
14	225	100.0	225	12	US-10-063-549-120
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16	225	100.0	225	12	US-10-063-551-120
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18	225	100.0	225	12	US-10-176-483-358
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20	225	100.0	225	12	US-10-176-914-358
21	225	100.0	225	12	US-10-176-915-358
22	225	100.0	225	12	US-10-006-485A-328
23	225	100.0	225	12	US-10-013-907A-328
24	225	100.0	225	12	US-10-015-499A-328
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27	225	100.0	225	12	US-10-063-594-120
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31	225	100.0	225	12	US-10-180-550-358
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33	225	100.0	225	12	US-10-187-738-358
34	225	100.0	225	12	US-10-187-740-358
35	225	100.0	225	12	US-10-187-883-358
36	225	100.0	225	12	US-10-194-363-358
37	225	100.0	225	12	US-10-194-460-358
38	225	100.0	225	12	US-10-194-463-358
39	225	100.0	225	12	US-10-194-484-358
40	225	100.0	225	12	US-10-195-884-358
41	225	100.0	225	12	US-10-195-896-358
42	225	100.0	225	12	US-10-196-744-358
43	225	100.0	225	12	US-10-196-755-358
44	225	100.0	225	12	US-10-196-757-358
45	225	100.0	225	12	US-10-197-704-358

ALIGNMENTS

RESULT 1
US-09-731-872-405
; Sequence 405, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US3 RRS
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 405
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-405

Query Match 100.0%; Score 225; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MATHALEIAGLFLGGVMVGTVAVTVPQWRVSATFENNVFVFENFWEGLMNCVRQANI	60
Db	1	MATHALEIAGLFLGGVMVGTVAVTVPQWRVSATFENNVFVFENFWEGLMNCVRQANI	60
QY	61	RMCKIYDLSLALSPDQAARGLMCAASVMSFLAFMAIILGMKCTRTGNEKVAHILL	120
Db	61	RMCKIYDLSLALSPDQAARGLMCAASVMSFLAFMAIILGMKCTRTGNEKVAHILL	120
QY	121	TAGIIFITGMVLLIPVSWVANAIIRDVNSIVNVAOKRELGEALYLCWTALVIYGGA	180

Fri Sep 3 10:15:54 2004

us-10-063-732-120.olg6.rapb

Db 121 TAGIIFITGMVVLIPVSWANALIRDFYNSIVNVAQKEELGEALYLGWTTALVLIVGGA 180

OY 181 LECVFCCKEKSSESSRYSTPSRRTTKSKSYHTGKSPSVYRSQYV 225

Db 181 LECVFCCKEKSSESSRYSTPSRRTTKSKSYHTGKSPSVYRSQYV 225

RESULT 2

US-09-946-374-328

; Sequence 328, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2830P1C1

; CURRENT APPLICATION NUMBER: US/09/946,374

; CURRENT FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

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; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/101738

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 60/101741

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 60/101743

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; PRIOR FILING DATE: 1998-09-24

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; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 60/102207

; PRIOR FILING DATE: 1998-09-29

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 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 60/102330
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 ; PRIOR APPLICATION NUMBER: 60/102331
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 ; PRIOR FILING DATE: 1998-10-26
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 ; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105807

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 DB 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNVVFNFWEGLMWNCVRQANI 60
 QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120

DB 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
 DB 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
 RESULT 3
 US-09-876-997-405
 ; Sequence 405, Application US/09876997
 ; Publication No. US20030152921A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, Jean Baptiste
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Jobert, Severin
 ; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
 ; FILE REFERENCE: 78 US4 CIP
 ; CURRENT APPLICATION NUMBER: US/09/876,997
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 09/731,872
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/187,470
 ; PRIOR FILING DATE: 2000-03-06
 ; PRIOR APPLICATION NUMBER: US 60/169,629
 ; PRIOR FILING DATE: 1999-12-08
 ; NUMBER OF SEQ ID NOS: 482
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 405
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-876-997-405

Query Match 100.0%; Score 225; DB 10; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1e-208;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNVVFNFWEGLMWNCVRQANI 60
 DB 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNVVFNFWEGLMWNCVRQANI 60
 QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120
 DB 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
 DB 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 4
 US-10-206-915-358
 ; Sequence 358, Application US/10206915
 ; Publication No. US20040029221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.

Fri Sep 3 10:15:54 2004

us-10-063-732-120.olig6.rapb

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; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-206-915-358

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFTENNIIVFENFEGLMNMCVRQANI 60
QY 61 RMCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 5
US-10-670-358
; Sequence 358, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/201,858
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-199-670-358

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFTENNIIVFENFEGLMNMCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFTENNIIVFENFEGLMNMCVRQANI 60
QY 61 RMCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDLSLLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCVFCCKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 6
US-10-201-858-358
; Sequence 358, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
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; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 358
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-201-858-358

Query Match 100.0%; Score 225; DB 12; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1e-208; Indels 0; Gaps 0;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATHALETAGLFGGVGMGTAVTVMPQWRVSAFIENNVVFENFWEGLMNCVROANI 60
 DB 1 MATHALETAGLFGGVGMGTAVTVMPQWRVSAFIENNVVFENFWEGLMNCVROANI 60
 QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMGFLAPMMAILGMKCTCTGDNKVKAHILL 120
 DB 61 RMCKIYDSLALSPDLQAARGLMCAASVMGFLAPMMAILGMKCTCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVLIPIVSWANAIIRDYFNSIVNVAQKREGLALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVLIPIVSWANAIIRDYFNSIVNVAQKREGLALYLGWTTALVIVGGA 180
 QY 181 LFCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225
 DB 181 LFCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225

RESULT 7
 US-10-205-890-358
 ; Sequence 358, Application US/10205890
 ; Publication No. US20040048334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C519
 ; CURRENT APPLICATION NUMBER: US/10/205,890
 ; PRIOR FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 358
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-205-890-358

Query Match 100.0%; Score 225; DB 12; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.1e-208; Indels 0; Gaps 0;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATHALETAGLFGGVGMGTAVTVMPQWRVSAFIENNVVFENFWEGLMNCVROANI 60
 DB 1 MATHALETAGLFGGVGMGTAVTVMPQWRVSAFIENNVVFENFWEGLMNCVROANI 60
 QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMGFLAPMMAILGMKCTCTGDNKVKAHILL 120
 DB 61 RMCKIYDSLALSPDLQAARGLMCAASVMGFLAPMMAILGMKCTCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVLIPIVSWANAIIRDYFNSIVNVAQKREGLALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVLIPIVSWANAIIRDYFNSIVNVAQKREGLALYLGWTTALVIVGGA 180
 QY 181 LFCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225
 DB 181 LFCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQVY 225

RESULT 8
 US-10-208-024-358
 ; Sequence 358, Application US/10208024
 ; Publication No. US20040048335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C538
 ; CURRENT APPLICATION NUMBER: US/10/208,024
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNIIVFENFWEGLMMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNIIVFENFWEGLMMNCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKSSSYRISPSHRTTKSYHTGKSPSVYRSQYV 225
Db 181 LFCCVFCCKSSSYRISPSHRTTKSYHTGKSPSVYRSQYV 225

RESULT 10
US-10-063-745-120
; Sequence 120, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Falvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-120

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNIIVFENFWEGLMMNCVRQANI 60

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 358
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-358

Query Match      100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNIIVFENFWEGLMMNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMGTVAVTMPQWRVSFAFIENNIIVFENFWEGLMMNCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKSSSYRISPSHRTTKSYHTGKSPSVYRSQYV 225
Db 181 LFCCVFCCKSSSYRISPSHRTTKSYHTGKSPSVYRSQYV 225

RESULT 9
US-10-201-853-358
; Sequence 358, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 11

US-10-063-512-120
; Sequence 120, Application US/10063512
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 12

US-10-063-513-120
; Sequence 120, Application US/10063513
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
Db 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKMKTRCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDYNSVNVQAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRISPSHRTTQKSYHTGKSPSVYSRSQYV 225

RESULT 13

US-10-063-515-120
; Sequence 120, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-120

Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTMPQWRVSAFIENNVFENFWGLWMCVRQANI 60

Fri Sep 3 10:15:54 2004

```
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 120
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-120
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Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTVPQWRVSAFIENNIIVFENFWEGLWMNCVQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTVPQWRVSAFIENNIIVFENFWEGLWMNCVQANI 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225

Search completed: September 1, 2004, 17:01:06
Job time : 50 secs
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Query Match 100.0%; Score 225; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATHALEIAGLFLGGVGMVGTVAVTVPQWRVSAFIENNIIVFENFWEGLWMNCVQANI 60
Db 1 MATHALEIAGLFLGGVGMVGTVAVTVPQWRVSAFIENNIIVFENFWEGLWMNCVQANI 60
QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVVLIPVSWANAIIRDFFNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
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RESULT 15
US-10-063-569-120
; Sequence 120, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
```


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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:56:09; Search time 42 Seconds
(without alignments)
1690.276 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGFLGGMVG.....QKSYHTGKSPVYSRSQV 225

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 6

Total number of hits satisfying chosen parameters: 2714

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12	5.3	209	13	Q90XR9	Q90xr9 brachydanio
2	9	4.0	214	13	Q90XR0	Q90xr0 brachydanio
3	9	4.0	214	13	Q98SR2	Q98sr2 gallus gall
4	9	4.0	216	13	Q98SR1	Q98sr1 gallus gall
5	9	4.0	224	11	Q8BXA6	Q8bxa6 mus musculu
6	8	3.6	213	13	Q80SG0	Q80sg0 xenopus lae
7	8	3.6	214	13	Q9DE12	Q9del2 xenopus lae
8	8	3.6	214	13	Q90XQ9	Q90xq9 xenopus lae
9	8	3.6	261	2	Q9L5U5	Q9l5u5 salmonella
10	8	3.6	265	16	Q9RG13	Q9rgt3 salmonella
11	8	3.6	311	17	Q8TQK4	Q8tqk4 methanosarc
12	8	3.6	393	16	Q89D52	Q89d52 bradyrhizob
13	8	3.6	459	16	Q81RJ5	Q81rj5 bacillus an
14	8	3.6	460	16	Q81EE6	Q81ee6 bacillus ce
15	8	3.6	536	4	Q9HB96	Q9hb96 homo sapien
16	8	3.6	686	3	O75013	O75013 schizosacch

17	8	3.6	1419	10	Q8LQEE6	Q8lqe6 oryza sativ
18	8	3.6	1607	16	Q89C03	Q89c03 bradyrhizob
19	7	3.1	22	2	Q56233	Q56233 thermus aqu
20	7	3.1	70	5	Q86KM9	Q86km9 dictyosteli
21	7	3.1	74	11	Q99KF8	Q99kf8 mus musculu
22	7	3.1	75	16	Q97FQ9	Q97fq9 clostridium
23	7	3.1	94	17	Q9HKT2	Q9hkt2 thermoplasma
24	7	3.1	133	10	Q8L8C7	Q8l8c7 ceratopteri
25	7	3.1	140	9	Q94WT4	Q94wt4 bacterioph
26	7	3.1	143	16	Q8XH76	Q8xh76 clostridium
27	7	3.1	148	2	Q7X509	Q7x509 streptomyce
28	7	3.1	148	16	Q8YTV2	Q8ytv2 anabaena sp
29	7	3.1	148	16	Q8PDJ7	Q8pdj7 xanthomonas
30	7	3.1	156	17	Q9Y9R3	Q9y9r3 aeropyrum p
31	7	3.1	167	16	Q9Z920	Q9z920 chlamydia p
32	7	3.1	169	2	Q9AEG4	Q9aeg4 enterobacte
33	7	3.1	169	16	Q9HWS4	Q9hws4 pseudomonas
34	7	3.1	177	16	Q81UB9	Q81ub9 bacillus an
35	7	3.1	178	16	Q8UJC1	Q8ujc1 agrobacteri
36	7	3.1	182	16	Q988I5	Q988i5 rhizobium l
37	7	3.1	184	8	Q85FL1	Q85fl1 adiantum ca
38	7	3.1	185	16	Q9K235	Q9k235 chlamydia p
39	7	3.1	186	5	Q8IDK0	Q8idk0 plasmodium
40	7	3.1	192	2	Q8RJ15	Q8rj15 methylococc
41	7	3.1	198	16	Q9L180	Q9l180 streptomyce
42	7	3.1	199	4	Q7Z4Y7	Q7z4y7 homo sapien
43	7	3.1	199	13	Q7ZTS2	Q7zts2 brachydanio
44	7	3.1	206	13	Q90XS1	Q90xs1 brachydanio
45	7	3.1	210	13	Q90XR4	Q90xr4 brachydanio

ALIGNMENTS

RESULT 1
Q90XR9
ID Q90XR9 PRELIMINARY; PRT; 209 AA.
AC Q90XR9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Claudin e.
GN CLDNE.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21417738; PubMed=11517306;
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
DR EMBL; AF359425; AAL01832.1; -;
DR ZFIN; ZDB-GENE-010328-5; cl dne.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR005411; Claudin2.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PRINTS; PR01589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN. 1.
SQ SEQUENCE 209 AA; 22593 MW; A86F48D852E16CB2 CRC64;

Query Match 5.3%; Score 12; DB 13; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 MOCKYDLSLL 73
 DB 62 MOCKYDLSLL 73

RESULT 2
 Q90XR0 PRELIMINARY; PRT; 214 AA.
 ID Q90XR0
 AC Q90XR0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin h.
 GN CLDNH.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21417736; PubMed=11517306;
 RA Kollmar R., Nakamura S.K., Kappeler J.A., Hudspeth A.J.;
 RT "Expression and phylogeny of claudins in vertebrate primordia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
 DR EMBL; AF359434; AAI01841.1; -;
 DR ZFIN; ZDB-GENE-010328-8; clndh.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 214 AA; 22788 MW; 38163AB7E50BF058 CRC64;

Query Match 4.0%; Score 9; DB 13; Length 214;
 Best Local Similarity 100.0%; Pred.No.1.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 46 WEGLMNVCV 54

RESULT 3
 Q98SR2 PRELIMINARY; PRT; 214 AA.
 ID Q98SR2
 AC Q98SR2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin-3.
 GN CLDN3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reardon E., Kojima S., Rizzolo L.J.;
 RT "Sequence of chick claudin-3 cDNA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF334677; AAK20876.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 4.0%; Score 9; DB 13; Length 216;
 Best Local Similarity 100.0%; Pred.No.1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 47 WEGLMNVCV 55

RESULT 4
 Q98SR1 PRELIMINARY; PRT; 216 AA.
 ID Q98SR1
 AC Q98SR1
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin-5.
 GN CLDN5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reardon E., Kojima S., Rizzolo L.J.;
 RT "Sequence of chick claudin-5 cDNA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF334678; AAK20877.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 4.0%; Score 9; DB 13; Length 216;
 Best Local Similarity 100.0%; Pred.No.1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 47 WEGLMNVCV 55

RESULT 5
 Q8BXA6 PRELIMINARY; PRT; 224 AA.
 ID Q8BXA6
 AC Q8BXA6
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to claudin-17.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

QY 62 MOCKYDLSLL 73
 DB 62 MOCKYDLSLL 73

RESULT 2
 Q90XR0 PRELIMINARY; PRT; 214 AA.
 ID Q90XR0
 AC Q90XR0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin h.
 GN CLDNH.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21417736; PubMed=11517306;
 RA Kollmar R., Nakamura S.K., Kappeler J.A., Hudspeth A.J.;
 RT "Expression and phylogeny of claudins in vertebrate primordia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
 DR EMBL; AF359434; AAI01841.1; -;
 DR ZFIN; ZDB-GENE-010328-8; clndh.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 214 AA; 22788 MW; 38163AB7E50BF058 CRC64;

Query Match 4.0%; Score 9; DB 13; Length 214;
 Best Local Similarity 100.0%; Pred.No.1.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 46 WEGLMNVCV 54

RESULT 3
 Q98SR2 PRELIMINARY; PRT; 214 AA.
 ID Q98SR2
 AC Q98SR2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin-3.
 GN CLDN3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reardon E., Kojima S., Rizzolo L.J.;
 RT "Sequence of chick claudin-3 cDNA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF334677; AAK20876.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 4.0%; Score 9; DB 13; Length 216;
 Best Local Similarity 100.0%; Pred.No.1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 47 WEGLMNVCV 55

RESULT 4
 Q98SR1 PRELIMINARY; PRT; 216 AA.
 ID Q98SR1
 AC Q98SR1
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Claudin-5.
 GN CLDN5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reardon E., Kojima S., Rizzolo L.J.;
 RT "Sequence of chick claudin-5 cDNA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF334678; AAK20877.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005923; C:tight junction; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN.
 DR SEQUENCE 216 AA; 23180 MW; 5037A882DFF5433A CRC64;

Query Match 4.0%; Score 9; DB 13; Length 216;
 Best Local Similarity 100.0%; Pred.No.1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMNVCV 55
 DB 47 WEGLMNVCV 55

RESULT 5
 Q8BXA6 PRELIMINARY; PRT; 224 AA.
 ID Q8BXA6
 AC Q8BXA6
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to claudin-17.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK048287; BAC33296.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin_reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 224 AA; 24653 MW; 6E049C863AB60A34 CRC64;

Query Match
Best Local Similarity 4.0%; Score 9; DB 11; Length 224;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 POWRVSAFI 36
Db 28 POWRVSAFI 36
|||||

RESULT 6
ID Q805G0 PRELIMINARY; PRT; 213 AA.
AC Q805G0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Claudin4L2.
GN CLDN4L2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26(2002).
DR EMBL; AB072909; BAC21014.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin_reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 213 AA; 22913 MW; ACF10FC95F9C16A1 CRC64;

Query Match
Best Local Similarity 3.6%; Score 8; DB 13; Length 213;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMWNC 54
Db 47 WEGLMWNC 54
|||||

RESULT 7
ID Q9DE12 PRELIMINARY; PRT; 214 AA.
AC Q9DE12;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transmembrane tight junction protein claudin.
GN CLA.

```

```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26(2002).
DR EMBL; AF359435; AAL01842.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin_reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 23151 MW; 3F0D65E3ADE311E6 CRC64;

Query Match
Best Local Similarity 3.6%; Score 8; DB 13; Length 214;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLMWNC 54
Db 47 WEGLMWNC 54
|||||

RESULT 8
ID Q90XQ9 PRELIMINARY; PRT; 214 AA.
AC Q90XQ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Claudin A (Claudin4L1).
GN CLDNA OR CLDN4L1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kollmar R., Nakamura S.K., Kappler J.A., Hudspeth A.J.;
RT "Expression and phylogeny of claudins in vertebrate primordia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10196-10201(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.;
RT "Gene expression pattern analysis of the tight junction protein,
RT Claudin, in the early morphogenesis of Xenopus embryos.";
RL Gene Expr. Patterns 2:23-26(2002).
DR EMBL; AF359435; AAL01842.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005923; C:tight junction; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin_reg.
DR InterPro; IPR004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
SQ SEQUENCE 214 AA; 22952 MW; 8E86F0EB2B72357D CRC64;

```

```

Query Match          3.6%; Score 8; DB 13; Length 214;
Best Local Similarity 100.0%; Pred. No. 17;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWNC 54
DB 47 WEGLWNC 54
|||||

RESULT 9
Q9LSU5 PRELIMINARY; PRT; 261 AA.
AC Q9LSU5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TrHE (Putative pilus assembly protein).
GN TrHE.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2028091; PubMed=10773089;
RA Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,
RA Grobeck E., Rose D.J., Taylor D.E.;
RT "The complete DNA sequence and analysis of R27, a large IncHI plasmid
RT from Salmonella typhi that is temperature sensitive for transfer.";
RL Nucleic Acids Res. 28:2177-2186(2000).
DR EMBL; AF250878; AAF69870.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 261 AA; 29233 MW; C1B2E63D3C86C16 CRC64;

Query Match          3.6%; Score 8; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 21;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPDLQA 79
DB 146 ALSPDLQA 153
|||||

RESULT 10
Q9RG73 PRELIMINARY; PRT; 265 AA.
AC Q9RG73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TrHE (Putative pilus assembly protein).
GN TrHE OR HCM1.70.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18; PLASMID=PHCM1;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebahia M.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AF105019; AAD54051.1; -.
DR EMBL; AL513383; CAD09678.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Complete proteome.
SQ SEQUENCE 265 AA; 29763 MW; AE66DB0C9CE9C7 CRC64;

Query Match          3.6%; Score 8; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 21;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPDLQA 79
DB 150 ALSPDLQA 157
|||||

RESULT 11
Q8TQK4 PRELIMINARY; PRT; 311 AA.
ID Q8TQK4;
AC Q8TQK4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein MA1538.
GN MA1538.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame J.A.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A., Smith K.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., de Macario E.C.,
RA Springer T.A., Umayam L.A., White O., White R.H., Paulsen I.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010823; AAM04952.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 311 AA; 34303 MW; 41E4C06862A4E410 CRC64;

Query Match          3.6%; Score 8; DB 17; Length 311;
Best Local Similarity 100.0%; Pred. No. 24;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 DSSLALSP 75
DB 230 DSSLALSP 237
|||||

RESULT 12
Q89D52 PRELIMINARY; PRT; 393 AA.
ID Q89D52;
AC Q89D52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Multidrug resistance efflux pump.
GN BLR7593.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005962; BAC52858.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015428; F:Type I protein secretor activity; IEA.
DR GO; GO:0003306; F:protein secretion; IEA.
DR InterPro; IPR006143; HlyD.
DR InterPro; IPR003997; RtxD.
DR Pfam; PF00529; HlyD; 1.
DR PRINTS; PR01490; RTXTOXIND.
KW Complete proteome.
SQ SEQUENCE 393 AA; 42533 MW; E40240F5E0D44E2 CRC64;

Query Match 3.6%; Score 8; DB 16; Length 393;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GDNKVK 116
DB 92 GDNKVK 99

RESULT 13
Q81RJ5 ID Q81RJ5 PRELIMINARY; PRT; 459 AA.
AC Q81RJ5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polysaccharide biosynthesis family protein.
GN BA2049.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017030; AAP25937.1; -.
DR TIGR; BA2049; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc_synt.

Query Match 3.6%; Score 8; DB 16; Length 460;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 MVVLIPVS 138
DB 297 MVVLIPVS 305

RESULT 14
Q81EE6 ID Q81EE6 PRELIMINARY; PRT; 460 AA.
AC Q81EE6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Export protein for polysaccharides and teichoic acids.
GN BC2034.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Shattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017004; AAP09003.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc_synt.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01943; Polysacc_synt; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Complete proteome.
SQ SEQUENCE 460 AA; 50684 MW; 8A5568EC9EB045E5 CRC64;

Query Match 3.6%; Score 8; DB 16; Length 460;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 MVVLIPVS 138
DB 298 MVVLIPVS 305

RESULT 15
Q9HB96 ID Q9HB96 PRELIMINARY; PRT; 536 AA.
AC Q9HB96
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fanconi anemia protein E (Fanconi anemia, complementation group E)
DE (DJ109F14.5).
GN FANCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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Fri Sep 3 10:15:55 2004

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RP SEQUENCE FROM N.A.
RX MEDLINE=20489873; PubMed=11001585;
RA de Winter J.P., Leveille F., van Berkel C.G.M., Rooimans M.A., N.,
RA van der Weel L., Steltenpool J., Demuth I., Morgan N.V., Alon N.,
RA Bosnyan-Collins L., Lightfoot J., Leeswater P.A., Waisfisz Q.,
RA Komatsu K., Arwert F., Pronk J.C., Mathew C.G., Digweed M.,
RA Buchwald M., Joenje H.;
RT "Isolation of a cDNA representing the Fanconi anemia complementation
RT group E gene.";
RL Am. J. Hum. Genet. 67:1306-1308 (2000) .
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF265210; AAG16743.1; -
DR EMBL; BC046359; AAH46359.1; -
DR EMBL; AL022721; CAD92504.1; -
DR Genew; HGNC:3596; FANCE.
DR GO; GO:0005634; C:nucleus; NAS.
SQ SEQUENCE 536 AA; 58710 MW; 0E94D8C469C791A5 CRC64;

Query Match 3.6%; Score 8; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LLALSPDL 77
Db 348 LLALSPDL 355

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Search completed: September 1, 2004, 16:59:28
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:56:30 ; Search time 16 Seconds
(without alignments)
1352.693 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALEIAGLFGVGMVG.....QKSHTGKKSPVYSRSQV 225

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1068

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	4.0	280	2 A39484	androgen-withdrawn
2	8	3.6	686	2 T39650	probable multifunc
3	7	3.1	22	2 T45268	hypothetical prote
4	7	3.1	75	2 D97228	hypothetical prote
5	7	3.1	115	2 T11448	NADH2 dehydrogenas
6	7	3.1	115	2 G89811	hypothetical prote
7	7	3.1	148	2 AD2132	hypothetical prote
8	7	3.1	156	2 E72531	hypothetical prote
9	7	3.1	167	2 B72112	hypothetical prote
10	7	3.1	167	2 D86511	hypothetical prote
11	7	3.1	169	2 A83134	hypothetical prote
12	7	3.1	178	2 AD2577	conserved hypotet
13	7	3.1	178	2 G97359	conserved hypotet
14	7	3.1	185	2 E81559	fxaA protein (VC26
15	7	3.1	213	2 C83772	hypothetical prote
16	7	3.1	215	2 A56168	hypothetical prote
17	7	3.1	238	2 B99789	deoxyadenosine kin
18	7	3.1	248	2 AC1919	conserved hypotet
19	7	3.1	253	2 S20738	hypothetical prote
20	7	3.1	253	2 B34801	chitinase (EC 3.2.
21	7	3.1	274	2 E83423	pathogenesis-relat
22	7	3.1	287	2 S74944	conserved hypotet
23	7	3.1	295	2 BE6653	hypothetical prote
24	7	3.1	330	2 AD2130	transmembrane lipo
25	7	3.1	351	1 S76613	N-acetyl-gamma-glu
26	7	3.1	352	2 AB2248	N-acetyl-glutamate
27	7	3.1	382	2 AF2994	glycosyltransferas
28	7	3.1	382	2 D98289	hypothetical prote
29	7	3.1	399	2 F83094	cell division prot

30 7 3.1 407 2 AE0121 probable membrane
31 7 3.1 427 2 E83530 hypothetical prote
32 7 3.1 442 2 T16773 hypothetical prote
33 7 3.1 443 2 D82975 two-component sens
34 7 3.1 450 2 A10909 probable membrane
35 7 3.1 451 2 S77599 probable coproporp
36 7 3.1 459 2 G82431 C4-dicarboxylate t
37 7 3.1 463 2 E81141 xanthine/uracil pe
38 7 3.1 465 2 T16835 hypothetical prote
39 7 3.1 482 2 E72882 conserved hypotet
40 7 3.1 487 2 C70574 glutamine syntheta
41 7 3.1 491 2 E69368 Probable sugar tra
42 7 3.1 499 2 AF0117 sodium/proton anti
43 7 3.1 500 2 F83418 CalB protein - Ara
44 7 3.1 510 2 T50526

ALIGNMENTS

RESULT 1 A39484

androgen-withdrawn apoptosis protein RVp1, prostatic - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000

C:Accession: A39484

R:Briehl, M.M.; Miesfeld, R.L.

Mol. Endocrinol. 5, 1381-1388, 1991

A:Title: Isolation and characterization of transcripts induced by androgen withdrawal ar

A:Reference number: A39484; MUID:92130987; PMID:1723140

A:Accession: A39484

A:Molecule type: mRNA

A:Residues: 1-280

A:Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858

C:Genetics:

A:Gene: RVP.1

C:Superfamily: rat androgen-withdrawn apoptosis protein RVP1

Query Match 4.0%; Score 9; DB 2; Length 280;

Best Local Similarity 100.0%; Pred. No. 0.58;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 WEGLWMNCV 55

Db 46 WEGLWMNCV 54

RESULT 2

T39650

probable multifunctional folic acid synthesis protein - fission yeast (Schizosaccharomyc

N:Alternate names: dihydropterate synthase

N:Contains: dihydropterate aldolase (EC 4.1.2.25); dihydropterate synthase (EC 2.5.1

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000

C:Accession: T39650; T40272

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z21868

A:Accession: T39650

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-686 <LYN>

A:Cross-references: EMBL:AL031856; PIDN:CAA21297.1; GSPDB:GN00067; SPDB:SPBC1734.03

A:Experimental source: strain 972h-; cosmid c1734

A:Accession: T40272

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-686 <LY2>

A:Cross-references: EMBL:AL031854; PIDN:CAA21289.1; GSPDB:GN00067; SPDB:SPBC337.19

A:Experimental source: strain 972h-; cosmid c337

C:Genetics:

A:Gene: SPBC1734.03; SPBC337.19

A;Map position: 2
 C;Superfamily: fasB-fasC-fasD multifunctional enzyme; 2-amino-4-hydroxy-6-hydroxymethyl
 C;Keywords: aldehyde-lyase; carbon-carbon lyase; transferase
 F:6-122/Domain: dihydroneopterin aldolase homology <DHA1>
 F:130-232/Domain: dihydroneopterin aldolase homology <DHA2>
 F:253-385/Domain: 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine pyrophosphokinase ho
 Query Match 3.6%; Score 8; DB 2; Length 686;
 Best Local Similarity 100.0%; Pred. No. 12; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 QY 70 LLALSPDL 77
 |||||
 Db 375 LLALSPDL 382
 |||||
 RESULT 3
 T45268
 hypothetical protein [imported] - Thermus aquaticus
 C;Species: Thermus aquaticus
 C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000
 C;Accession: T45268
 R;Motohima, H.; Minagawa, E.; Tsukasaki, F.; Kaminogawa, S.
 J. Ferment. Bioeng. 86, 21-27, 1998
 A;Title: Cloning and nucleotide sequencing of genes encoding Mn-superoxide dismutase and
 A;Reference number: Z22952
 A;Accession: T45268
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-22 <MOT>
 A;Cross-references: EMBL:D84646; PIDN:BAAL2701.1
 A;Experimental source: strain YT-1

Query Match 3.1%; Score 7; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 172 ALVLIVG 178
 |||||
 Db 10 ALVLIVG 16
 |||||
 RESULT 4
 D97228
 hypothetical protein CAC2668 [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C;Accession: D97228
 R;Nollig, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A;Reference number: A36900; MUID:21359325; PMID:21359325
 A;Accession: D97228
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-75 <XUR>
 A;Cross-references: GB:AE001437; PIDN:AAK90615.1; PID:gl5025698; GSPDB:GN00168
 A;Experimental source: Clostridium acetobutylicum ATCC824

Query Match 3.1%; Score 7; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 20; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 5 ALEIAGL 11
 |||||
 Db 4 ALEIAGL 10
 |||||

RESULT 5

T11448
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - nine-banded armadillo mitochondr
 C;Species: mitochondrion Dasypus novemcinctus (nine-banded armadillo)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
 C;Accession: T11448
 R;Arnason, U.; Gullberg, A.; Janke, A.
 Mol. Biol. Evol. 14, 762-768, 1997
 A;Title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship
 A;Reference number: Z17272; MUID:97357423; PMID:9214749
 A;Accession: T11448
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-115 <ARN>
 A;Cross-references: EMBL:Y11832; NID:g2252500; PIDN:CAA72523.1; PID:g225252508
 C;Genetics:
 A;Gene: NADH3
 A;Genome: mitochondrion
 A;Genetic code: SGCI
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 3.1%; Score 7; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 28; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 170 TTALVLI 176
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 Db 89 TTALVLI 95
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RESULT 6
 G69811
 hypothetical protein yf1t - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C;Accession: G69811
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
 Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69811
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-115 <KUN>
 A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12584.1; PID:g26330799

A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yf1t
 C;Superfamily: Bacillus subtilis hypothetical protein yf1t

Query Match 3.1%; Score 7; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 28; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 110 DNEKVK 116
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 Db 107 DNEKVK 113
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RESULT 7
AD2132

hypothetical protein all2611 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AD2132
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2132
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA074310.1; PID:G17131704; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all2611

Query Match 3.1%; Score 7; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ALSPLDQ 78
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 Db 51 ALSPLDQ 57

RESULT 8
 E72531
 hypothetical protein APE2225 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: E72531
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hailkawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kikuchi, Y.
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A:Reference number: A72450; MUID:99310339; PMID:10382965
 A:Accession: E72531
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:G5105654; PIDN:BA081237.1; PID:d1045023; PID:G5105654
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2225

Query Match 3.1%; Score 7; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 KRELGEA 164
 |||||
 Db 150 KRELGEA 156

RESULT 9
 B72112
 hypothetical protein - Chlamydomophila pneumoniae (strain CWL029)
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C:Accession: B72112
 R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: B72112
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-167 <ARN>
 A:Cross-references: GB:AE001603; GB:AE001363; NID:G4376422; PIDN:AA18317.1; PID:G437643
 A:Experimental source: strain CWL029

C:Genetics:

A:Gene: CPn0164

Query Match

3.1%; Score 7; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LIVGGAL 181

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Db 47 LIVGGAL 53

RESULT 10

D86511

hypothetical protein CPj0164 [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001

C:Accession: D86511

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: D86511

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-167 <STO>

A:Cross-references: GB:BA000008; NID:G8978537; PIDN:BA098374.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: CPj0164

Query Match

3.1%; Score 7; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LIVGGAL 181

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Db 47 LIVGGAL 53

RESULT 11

A83134

conserved hypothetical protein PA4104 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83134

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: A83134

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-169 <STO>

A:Cross-references: GB:AE004826; GB:AE004091; NID:G9950296; PIDN:AAG07491.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4104

Query Match

3.1%; Score 7; DB 2; Length 169;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 TALVLIIV 177

|||||

Db 93 TALVLIIV 99

RESULT 12

AH2577

conserved hypothetical protein fxSA [imported] - Agrobacterium tumefaciens (strain C58, ;

Fri Sep 3 10:15:54 2004

us-10-063-732-120.olig6.rpr

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2577
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2577
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <KUR>
A;Cross-references: GB:AE008698; PIDN:AA141038.1; PID:G17738323; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fxaA
A;Map position: circular chromosome
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 3.1%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 LGGVGMV 19
DB 50 LGGVGMV 56

RESULT 13
G97359
fxsA protein (VC2696) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: G97359
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <KUR>
A;Cross-references: GB:AE007869; PIDN:AXK5832.1; PID:G15154865; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C.11
A;Map position: circular chromosome
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 3.1%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 LGGVGMV 19
DB 50 LGGVGMV 56

RESULT 14
E81559
Hypothetical protein CP0607 [imported] - Chlamydomonas pneumoniae (strain AR39)
C;Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
R;Accession: E81559
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwynn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81559

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <REA>
A;Cross-references: GB:AE002218; GB:AE002161; NID:G1789509; PIDN:AAF38423.1; PID:G178951
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0607
Query Match 3.1%; Score 7; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 LIVGGAL 181
DB 65 LIVGGAL 71

RESULT 15
CB3772
hypothetical protein BH0979 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: CB3772
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: AB3650; MUID:20512582; PMID:11058132
A;Accession: CB3772
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:G10173440; PIDN:BAB04698.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0979

Query Match 3.1%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 118 ILTAGI 124
DB 73 ILTAGI 79

Search completed: September 1, 2004, 16:59:49
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 16:55:44 ; Search time 12 Seconds
(without alignments)
976.315 Million cell updates/sec

Title: US-10-063-732-120
Perfect score: 225
Sequence: 1 MATHALETAGLEPLGVGMVG.....QKSYHTGKSPSVGRSQVY 225

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 6

Total number of hits satisfying chosen parameters: 608

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	100.0	225	1	CLD8_HUMAN
2	13	5.8	225	1	CLD8_MOUSE
3	10	4.4	208	1	CLD7_ERARE
4	9	4.0	209	1	CLD4_CERAE
5	9	4.0	209	1	CLD4_HUMAN
6	9	4.0	210	1	CLD4_MOUSE
7	9	4.0	218	1	CLD3_CANFA
8	9	4.0	219	1	CLD3_MOUSE
9	9	4.0	219	1	CLD3_RAT
10	9	4.0	220	1	CLD3_HUMAN
11	8	3.6	224	1	CLD8_HUMAN
12	7	3.1	115	1	G17M_BACSU
13	7	3.1	115	1	N33M_DASNO
14	7	3.1	191	1	CLD7_RAT
15	7	3.1	209	1	CLD2_ERARE
16	7	3.1	211	1	CLD7_HUMAN
17	7	3.1	211	1	CLD7_MOUSE
18	7	3.1	211	1	CLD7_HUMAN
19	7	3.1	211	1	CLD7_MOUSE
20	7	3.1	214	1	DGK1_LACAC
21	7	3.1	215	1	CLD8_ERARE
22	7	3.1	217	1	CLD9_HUMAN
23	7	3.1	217	1	CLD9_MOUSE
24	7	3.1	219	1	CLD6_MOUSE
25	7	3.1	220	1	CLD6_HUMAN
26	7	3.1	230	1	CLD2_CANFA
27	7	3.1	230	1	CLD2_HUMAN
28	7	3.1	230	1	CLD2_MOUSE
29	7	3.1	239	1	CLD6_HUMAN
30	7	3.1	239	1	CLD6_MOUSE
31	7	3.1	253	1	CHIQ_TORAC
32	7	3.1	274	1	NAGB_FUSNN
33	7	3.1	278	1	KSGA_METKA

34	7	3.1	287	1	BTPA_SYNY3
35	7	3.1	295	1	LPIC_BACSU
36	7	3.1	312	1	XERC_RHLO
37	7	3.1	351	1	ARGC_SYNY3
38	7	3.1	352	1	ARCI_ANASP
39	7	3.1	352	1	ARGC_NOSEL
40	7	3.1	354	1	VATC_HORVU
41	7	3.1	443	1	PHOR_PSEAE
42	7	3.1	451	1	HEMN_PARDE
43	7	3.1	459	1	DCUC_VIBCH
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72966 synchocyst
P39129 bacillus su
Q98609 rhizobium 1
P54999 synchocyst
O8YTB1 anabaena sp
O87890 nostoc elli
Q9SCB9 hordeum vul
P23621 pseudomonas
Q51676 paracoccus
Q0K1S6 vibrio chol
O06297 mycobacteri
O29313 archaeoglob

287 3.1 BTPA_SYNY3
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451 3.1 HEMN_PARDE
459 3.1 DCUC_VIBCH
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225 AA.

STANDARD; PRT;

30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cladin-8.
CLDN8.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Keen T.J., Inglehearn C.F.;
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[1]
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MEDLINE=20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
Soda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Pooley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuoyama S., Antonakis S.E.,
Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P.,
Scharfe M., Beck A., Desario A., Reichelt J., Kauer G., Bloeker H.,
Ramsay J., Borzov K., Gardiner K., Hennig S., Riessmann L., Dagand E.,
Wehrach H., Reinhardt R., Yaspo M.-L.,
Lehrach H., Reinhardt R., Yaspo M.-L.,
"The DNA sequence of human chromosome 21."
Nature 405:311-319(2000).
[3]
SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length

ALIGNMENTS

```

RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ250711; CAB60615.1; -
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DR EMBL; BC058004; AAH58004.1; -
DR Genbank; HGNC:2050; CLDN8.
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DR Pfam; PF00822; PMP22 Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
DR TIGHT junction; Transmembrane.
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DB 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMALLGMKTRCTGDKNEKVKAHLL 120
QY 121 TAGIIFITGTGVLIPVSWANAIIRDFYNSVNAOKRELGEALYLGTWTLVLIYVGA 180
DB 121 TAGIIFITGTGVLIPVSWANAIIRDFYNSVNAOKRELGEALYLGTWTLVLIYVGA 180
QY 181 LFCVFCCKNEKSSSVYRISPSHRTTQKSYHTGKKSPPSVYSRQYV 225
DB 181 LFCVFCCKNEKSSSVYRISPSHRTTQKSYHTGKKSPPSVYSRQYV 225

RESULT 2
CLD8 MOUSE STANDARD; PRT; 225 AA.
AC Q92260;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-8.
GN CLDN8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99110921; PubMed=9892664;
RA Morita K., Furuse M., Fujimoto K., Tsukita S.;
RT "Claudin multigene family encoding four-transmembrane domain protein
RT components of tight junction strands."
RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).

[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Breast tumor;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF087826; AAD09761.1; -
DR EMBL; BC003868; AAH03868.1; -
DR MGD; MGI:1859286; Clnd8.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
DR TIGHT junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
SQ SEQUENCE 225 AA; 24947 MW; 12BB3C460F23D876 CRC64;

Query Match 5.8%; Score 13; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGGVGVGVGTAVT 25
DB 13 LGGVGVGVGTAVT 25

RESULT 3
CLDY BRARE STANDARD; PRT; 208 AA.
ID CLDY BRARE
AC Q9VH91;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-like protein ZF-A99.
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

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OX NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RA Keen R.J., Inglehearn C.F.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF011789; CAA09777.1; --
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR005411; Claudin2.
DR InterPro; IPR006188; Claudin_reg.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PRINTS; PR01589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 208 AA; 22205 MW; 6A4BB5EBF3C0AB81 CRC64;

Query Match 4.4%; Score 10; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 FWEGLWMNCV 55
DB |||||

RESULT 4
CLD4_CERAE STANDARD; PRT; 209 AA.
AC O19005;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
DE receptor) (CPE-R).
GN CLD4 OR CPETR1 OR CPER.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9724241; PubMed=9087440;
RA Katakura J., Inoue N., Horiguchi Y., Matsuda M., Sugimoto N.;
RT "Molecular cloning and functional characterization of the receptor for
RT Clostridium perfringens enterotoxin."
RL J. Cell Biol. 136:1239-1247(1997).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF011789; CAA09777.1; --
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR005411; Claudin2.
DR InterPro; IPR006188; Claudin_reg.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PRINTS; PR01589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 208 AA; 22205 MW; 6A4BB5EBF3C0AB81 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
DB |||||

RESULT 5
CLD4_HUMAN STANDARD; PRT; 209 AA.
AC O14493;
DT 30-MAY-2000 (Rel. 39, Created)
DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
DE receptor) (CPE-R) (Williams-Beuren syndrome chromosome region 8
DE protein).
GN CLD4 OR CPETR1 OR CPER OR WBSR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal brain;
RX MEDLINE=97476271; PubMed=9334247;
RA Katakura J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M.,
RA Sugimoto N.;
RT "Clostridium perfringens enterotoxin utilizes two structurally related
RT membrane proteins as functional receptors in vivo."
RL J. Biol. Chem. 272:26652-26658(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."

```

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Component of tight junction (TJ) strands.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Haploinsufficiency of CLDN4 may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
 CC is a contiguous gene deletion syndrome involving genes from
 CC chromosome band 7q11.23.
 CC -!- SIMILARITY: Belongs to the claudin family.
 CC
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 CC
 CC EMBL; AB000713; BAA22984.1; -;
 CC EMBL; AF087822; AAD09757.1; -;
 CC MGD; MGI:131314; Cldn4.
 CC InterPro; IPR006187; Claudin.
 CC InterPro; IPR004031; PMP22_Claudin.
 CC Pfam; PF00822; PMP22_Claudin; 1.
 CC PRINTS; PR01077; CLAUDIN.
 CC PROSITE; PS01346; CLAUDIN; 1.
 CC Tight junction; Transmembrane.
 CC TRANSMEM 8 28 POTENTIAL.
 CC TRANSMEM 82 102 POTENTIAL.
 CC TRANSMEM 117 137 POTENTIAL.
 CC TRANSMEM 161 181 POTENTIAL.
 CC SEQUENCE 210 AA; 22338 MW; 3B6D571EC71D6564 CRC64;
 CC
 CC Query Match 4.0%; Score 9; DB 1; Length 210;
 CC Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 CC Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 47 WEGLMWNCV 55
 CC Db 47 WEGLMWNCV 55
 CC
 CC RESULT 7
 CC CLD3_CANFA STANDARD; PRT; 218 AA.
 CC ID CLD3_CANFA
 CC AC Q95KM5;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Claudin-3.
 CC GN CLDN3.
 CC OS Canis familiaris (Dog).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC OX NCBI_TaxID=9615;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=21206012; PubMed=11309408;
 CC RA Furuse M., Furuse K., Sasaki H., Tsukita S.;
 CC RT "Conversion of zonulae occludentes from tight to leaky strand type by
 CC introducing claudin-2 into Madin-Darby canine kidney I cells.";
 CC RL J. Cell Biol. 153:263-272(2001).
 CC CC -!- FUNCTION: Component of tight junction (TJ) strands.
 CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC CC -!- SIMILARITY: Belongs to the claudin family.
 CC
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Component of tight junction (TJ) strands.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Haploinsufficiency of CLDN4 may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
 CC is a contiguous gene deletion syndrome involving genes from
 CC chromosome band 7q11.23.
 CC -!- SIMILARITY: Belongs to the claudin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB000712; BAA22984.1; -;
 CC EMBL; BC000671; AAB00671.1; -;
 CC Genew; HGNC:2046; CLDN4.
 CC MIM; 602909; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
 CC GO; GO:0009405; P:pathogenesis; TAS.
 CC InterPro; IPR006187; Claudin.
 CC InterPro; IPR006188; Claudin_reg.
 CC InterPro; IPR004031; PMP22_Claudin.
 CC Pfam; PF00822; PMP22_Claudin; 1.
 CC PRINTS; PR01077; CLAUDIN.
 CC PROSITE; PS01346; CLAUDIN; 1.
 CC Tight junction; Transmembrane; Williams-Beuren syndrome.
 CC TRANSMEM 8 28 POTENTIAL.
 CC TRANSMEM 82 102 POTENTIAL.
 CC TRANSMEM 118 138 POTENTIAL.
 CC TRANSMEM 161 181 POTENTIAL.
 CC SEQUENCE 209 AA; 22077 MW; 0659A93AA5F0E4C5 CRC64;
 CC
 CC Query Match 4.0%; Score 9; DB 1; Length 209;
 CC Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 CC Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 47 WEGLMWNCV 55
 CC Db 47 WEGLMWNCV 55
 CC
 CC RESULT 6
 CC CLD4_MOUSE STANDARD; PRT; 210 AA.
 CC ID CLD4_MOUSE
 CC AC O35054;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
 CC receptor) (CPE-R).
 CC GN CLDN4 OR CPER1 OR CPER.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=97476271; PubMed=9334247;
 CC RA Katsuhira J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M.,
 CC RA Sugimoto N.;
 CC RT "Clostridium perfringens enterotoxin utilizes two structurally related
 CC membrane proteins as functional receptors in vivo.";
 CC RL J. Biol. Chem. 272:26652-26658(1997).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=99110921; PubMed=9892664;
 CC RA Morita K., Furuse M., Fujimoto K., Tsukita S.;

```

DR EMBL; AF358908; AAK51434.1; --
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin. reg.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN.
KW Tight junction; Transmembrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 218 AA; 23148 MW; 907104E36F50DA70 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db |||||
46 WEGLWMNCV 54

RESULT 8
CLD3 MOUSE
ID CLD3 MOUSE STANDARD; PRT; 219 AA.
AC Q9Z0G9; Q91X40;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE-
DE receptor 2) (CPE-R 2).
GN CLDN3 OR CPE2R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99097345; PubMed=9878248;
RA Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;
RT "Genes for the CPE receptor (CPE2R1) and the human homolog of RVP1
RT (CPE2R2) are localized within the Williams-Beuren syndrome deletion.";
RL Genomics 54:453-459(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99110921; PubMed=9892664;
RA Morita K., Furuse M., Fujimoto K., Tsukita S.;
RT "Claudin multigene family encoding four-transmembrane domain protein
RT components of tight junction strands.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

```

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RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Z0G9-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Z0G9-2; Sequence=VSP_001101;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the claudin family.
CC
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CC
CC EMBL; AF095905; AAD14608.1; --
CC EMBL; AF087821; AAD09756.1; --
CC EMBL; BC012650; AAI12650.1; --
CC MGD; MGI:1329044; Cldn3.
CC InterPro; IPR006187; Claudin.
CC InterPro; IPR006188; Claudin. reg.
CC Pfam; PF00822; PMP22 Claudin.
CC PRINTS; PR01077; CLAUDIN.
CC PROSITE; PS01346; CLAUDIN.
KW Tight junction; Transmembrane; Alternative splicing.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT VARSPLIC 72 91 Missing (in isoform 2).
FT /FTID=VSP_001101.
SQ SEQUENCE 219 AA; 23284 MW; 62F67810D9B9BD37 CRC64;

Query Match 4.0%; Score 9; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 WEGLWMNCV 55
Db |||||
46 WEGLWMNCV 54

RESULT 9
CLD3 RAT
ID CLD3 RAT STANDARD; PRT; 219 AA.
AC Q63400;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-3 (Ventral prostate.1 protein) (RVF1).
GN CLDN3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92130987; PubMed=1723140;
RA Briel M.M., Miesfeld R.L.;
RT "Isolation and characterization of transcripts induced by androgen
RT withdrawal and apoptotic cell death in the rat ventral prostate.";
RL Mol. Endocrinol. 5:1381-1388(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

```

```

CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
CC EMBL; M74067; AAA41760.1; -.
CC EMBL; AJ011656; CAA09727.1; -.
CC InterPro; IPR006187; Claudin.
CC InterPro; IPR006188; Claudin reg.
CC Pfam; PF00822; PMP22_Claudin; 1.
CC PRINTS; PR01077; CLAUDIN
CC PROSITE; PS01346; CLAUDIN; 1.
CC Tight junction; Transmembrane.
CC TRANSMEM 9 29 POTENTIAL.
CC TRANSMEM 81 101 POTENTIAL.
CC TRANSMEM 116 136 POTENTIAL.
CC TRANSMEM 162 182 POTENTIAL.
CC G->S (IN REF. 1).
CC MISSING (IN REF. 1).
CC DYV -> TTSRPGARTPHHHVQPSMYPTRPACSLASETT
CC PPSRRLLQTPRSLLARLEDRQGVFPSPVAT (IN REF.
CC 1).
CC SEQUENCE 219 AA; 23314 MW; 820CC6BFC20D122D CRC64;
CC -----
CC Query Match 4.0%; Score 9; DB 1; Length 219;
CC Best Local Similarity 100.0%; Pred. No. 0.15;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
Cc 47 WEGLWMNCV 55
Cc |||||
Cc 46 WEGLWMNCV 54
Cc -----
Cc RESULT 10
Cc CLD3_HUMAN
Cc ID CLD3_HUMAN STANDARD; PRT; 220 AA.
Cc AC O1551;
Cc DT 30-MAY-2000 (Rel. 39, Created)
Cc DT 30-MAY-2000 (Rel. 39, Last sequence update)
Cc DT 10-OCT-2003 (Rel. 42, Last annotation update)
Cc DE Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE-
Cc DE receptor 2) (CPE-R 2) (Ventral prostate.1 protein homolog) (HRVP1).
Cc GN CLDN3 OR CPEPR2.
Cc OS Homo sapiens (Human).
Cc OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Cc OX NCBI_TaxID=9606;
Cc RN [1]
Cc RP SEQUENCE FROM N.A.
Cc RX MEDLINE=98110580; PubMed=9441748;
Cc RA Peacock R.H., Keen T.J., Inglehearn C.F.;
Cc RT "Analysis of a human gene homologous to rat ventral prostate.1
Cc RT protein."
Cc RL Genomics 46:443-449(1997).
Cc RN [2]
Cc RP SEQUENCE FROM N.A.
Cc RX MEDLINE=97476271; PubMed=9334247;
Cc RA Katakura J., Sugiyama H., Inoue N., Horiguchi Y., Matsuda M.,
Cc RA Sugimoto N.;
Cc RT "Clostridium perfringens enterotoxin utilizes two structurally related
Cc RT membrane proteins as functional receptors in vivo."
Cc RL J. Biol. Chem. 272:26652-26658(1997).
Cc RN [3]
Cc RP SEQUENCE FROM N.A.
Cc RT TISSUE=Colon;

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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullany S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."; 16999-16903(2002).
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -!- FUNCTION: Component of tight junction (TJ) strands.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DISEASE: Haploinsufficiency of CLDN3 may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC -!- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
Cc EMBL; AF007189; AAC78277.1; -.
Cc EMBL; AB000714; BAA22986.1; -.
Cc EMBL; BC016056; AAI16056.1; -.
Cc Genew; HGNC:2045; CLDN3.
Cc MIM; 602910; -.
Cc GO; GO:0005887; C: integral to plasma membrane; TAS.
Cc GO; GO:0004888; F: transmembrane receptor activity; TAS.
Cc InterPro; IPR006187; Claudin.
Cc InterPro; IPR006188; Claudin reg.
Cc InterPro; IPR004031; PMP22_Claudin.
Cc Pfam; PF00822; PMP22_Claudin; 1.
Cc PRINTS; PR01077; CLAUDIN.
Cc PROSITE; PS01346; CLAUDIN; 1.
Cc Tight junction; Transmembrane; Williams-Beuren syndrome.
Cc TRANSMEM 9 29 POTENTIAL.
Cc TRANSMEM 81 101 POTENTIAL.
Cc TRANSMEM 116 136 POTENTIAL.
Cc TRANSMEM 160 180 POTENTIAL.
Cc SEQUENCE 220 AA; 23318 MW; 1C826EFFF1563C56 CRC64;
Cc -----
Cc Query Match 4.0%; Score 9; DB 1; Length 220;
Cc Best Local Similarity 100.0%; Pred. No. 0.15;
Cc Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cc -----
Cc 47 WEGLWMNCV 55
Cc |||||
Cc 46 WEGLWMNCV 54
Cc -----
Cc RESULT 11
Cc CLD3_HUMAN
Cc ID CLD3_HUMAN STANDARD; PRT; 224 AA.
Cc AC P56750;
Cc DT 30-MAY-2000 (Rel. 39, Created)
Cc DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE CLDN17.
 GN CLDN17.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Keen T.J., Ingleharn C.F.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Reichwald K., Rump A., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramer J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Vaspo M.-L.;
 RL "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 CC -!- FUNCTION: Component of tight junction (TJ) strands.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the claudin family.
 CC -----
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 CC -----
 DR EMBL; AJ250712; CAB60616.1; -;
 DR EMBL; AP001707; BAA95566.1; -;
 DR Genbank; HGNC:2038; CLDN17.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN; 1.
 DR TIGR; TIGR00000; Transmembrane.
 KW TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 125 145 POTENTIAL.
 FT TRANSMEM 165 185 POTENTIAL.
 SQ SEQUENCE 224 AA; 24603 MW; 1833ED3178B7F63A CRC64;

 Query Match 3.6%; Score 8; DB 1; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 28 POWRVSAF 35
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 Db 28 POWRVSAF 35

 RESULT 12
 GI7M_BACSU STANDARD; PRT; 115 AA.
 AC P80241;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE General stress protein 17M (GSP17M).

GN YFLT OR BSU07550.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamanoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
 RL "Cloning and sequencing of a 35.7 Kb in the 70 degree-73 degree region
 of the Bacillus subtilis genome reveal genes for a new two-component
 system, three spore germination proteins, an iron uptake system and a
 general stress response protein.";
 RL Gene 194:191-199(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97417488; PubMed=9272861;
 RA Yamanoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
 RL "Cloning and sequencing of a 35.7 Kb in the 70 degree-73 degree region
 of the Bacillus subtilis genome reveal genes for a new two-component
 system, three spore germination proteins, an iron uptake system and a
 general stress response protein.";
 RL Gene 194:191-199(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche E., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenberg M., Vannier P., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamanoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RL "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX STRAIN=168 / IS58;
 MEDLINE=94282319; PubMed=8012595;
 RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
 RA Schmid R., Mach H., Hecker M.;
 RL "Analysis of the induction of general stress proteins of Bacillus
 subtilis";
 RL Microbiology 140:741-752(1994).
 CC -!- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
 CC -!- limitation and oxygen limitation.
 CC -----
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 CC -----
 DR EMBL; D86417; BAA22314.1; -;
 DR EMBL; Z99108; CAB12584.1; -;
 DR FIR; G69811; G69811.
 DR Subtilist; BG19020; yflt.

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KW Heat shock; Complete proteome.
SQ SEQUENCE 115 AA; 13112 MW; 6D25F4637C55779A CRC64;

Query Match      3.1%; Score 7; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 DNEKYKA 116
DB 107 DNEKYKA 113

RESULT 13
NU3M_DASNO STANDARD; PRT; 115 AA.
ID NU3M_DASNO
AC O21332;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).
GN MTND3 OR ND3 OR NADH3.
OS Dasytus novemcinctus (Nine-banded armadillo).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Dasytus.
OC NCBI_TaxID=9361;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97357423; PubMed=9214749;
RA Arnason U., Gullberg A., Janke A.;
RT "Phylogenetic analyses of mitochondrial DNA suggest a sister group
RT relationship between Xenarthra (Edentata) and Ferungulates.";
RL Mol. Biol. Evol. 14:762-768(1997).
CC -|- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -|- SIMILARITY: Belongs to the complex I subunit 3 family.
CC
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CC
CC EMBL; Y11832; CAA72523.1; -.
DR PIR; T11448; T11448.
DR InterPro; IPR000440; Oxidored g4.
DR Pfam; PF00507; oxidored g4; 1.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
KW SEQUENCE 115 AA; 13034 MW; 397E1705EB92E571 CRC64;
SQ SEQUENCE 115 AA; 13034 MW; 397E1705EB92E571 CRC64;

Query Match      3.1%; Score 7; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 TVALVI 176
DB 89 TVALVI 95

RESULT 14
CLD7_RAT STANDARD; PRT; 191 AA.
ID CLD7_RAT
AC Q9Z1L1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-7 (Fragment).
GN CLDN7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;

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RN SEQUENCE FROM N.A.
RP Keen T.J., Inglehearn C.F.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Component of tight junction (TJ) strands.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the claudin family.
CC
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CC
CC EMBL; AJ011811; CAA09790.1; -.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR Pfam; PF004031; PMP22_Claudin.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT SEQUENCE 191 AA; 20366 MW; 83B445908DFF41A CRC64;
SQ SEQUENCE 191 AA; 20366 MW; 83B445908DFF41A CRC64;

Query Match      3.1%; Score 7; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GMKCTRC 107
DB 81 GMKCTRC 87

RESULT 15
CLDZ_BRARE STANDARD; PRT; 209 AA.
ID CLDZ_BRARE
AC Q9YH90;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-like protein ZF-A9.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Inglehearn C.F.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Component of tight junction (TJ) strands.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the claudin family.
CC
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CC
CC EMBL; AJ011790; CAA09778.1; -.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin reg.
DR Pfam; PF00822; PMP22_Claudin; 1.

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DR PRINTS: PR01077: CLAUDIN.
DR PROSITE: PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 114 134 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
SQ SEQUENCE 209 AA; 22091 MW; C413143811853D58 CRC64;

Query Match
Best Local Similarity 3.1%; Score 7; DB 1; Length 209;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 IIRDFYN 150
Db 142 IIRDFYN 148

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Job time : 14 secs

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PR	17-SEP-1998;	98US-0100684P.	PR	03-NOV-1998;	98US-0106919P.	PA	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PR	17-SEP-1998;	98US-0100710P.	PR	03-NOV-1998;	98US-0106932P.	XX	WPI; 2000-237871/20.
PR	17-SEP-1998;	98US-0100711P.	PR	03-NOV-1998;	98US-0106934P.	DR	N-PSDB; AAA37115.
PR	17-SEP-1998;	98US-0100919P.	PR	10-NOV-1998;	98US-0107783P.	XX	New mammalian DNA sequences encoding transmembrane, receptor or secreted
PR	17-SEP-1998;	98US-0100930P.	PR	17-NOV-1998;	98US-0108775P.	PT	PRO polypeptides, useful for screening of potential peptide or small
PR	18-SEP-1998;	98US-0100848P.	PR	17-NOV-1998;	98US-0108779P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.
PR	18-SEP-1998;	98US-0100849P.	PR	17-NOV-1998;	98US-0108787P.	XX	Claim 12; Fig 188; 773pp; English.
PR	18-SEP-1998;	98US-0101014P.	PR	17-NOV-1998;	98US-0108801P.	XX	AAA37022 to AAA37144 encode the new isolated human transmembrane,
PR	18-SEP-1998;	98US-0101068P.	PR	17-NOV-1998;	98US-0108806P.	CC	receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
PR	18-SEP-1998;	98US-0101071P.	PR	17-NOV-1998;	98US-0108807P.	CC	transmembrane and receptor PRO proteins can be used for screening of
PR	22-SEP-1998;	98US-0101279P.	PR	17-NOV-1998;	98US-0108808P.	CC	potential peptide or small molecule inhibitors of the relevant
PR	23-SEP-1998;	98US-0101472P.	PR	17-NOV-1998;	98US-0108809P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences
PR	23-SEP-1998;	98US-0101473P.	PR	17-NOV-1998;	98US-0108810P.	CC	encoding then have various industrial applications, including uses as
PR	23-SEP-1998;	98US-0101476P.	PR	18-NOV-1998;	98US-0108849P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
PR	23-SEP-1998;	98US-0101477P.	PR	18-NOV-1998;	98US-0108850P.	CC	primers and hybridisation probes used in the isolation of the PRO
PR	23-SEP-1998;	98US-0101479P.	PR	18-NOV-1998;	98US-0108851P.	CC	polypeptides from the present invention
PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.	XX	Sequence 225 AA;
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.	XX	Query Match 100.0%; Score 225; DB 3; Length 225;
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.	XX	Best Local Similarity 100.0%; Pred. No. 3.2e-212; Indels 0; Gaps 0;
PR	24-SEP-1998;	98US-0101915P.	XX			XX	Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	24-SEP-1998;	98US-0101916P.	XX			XX	QY 1 MATHALEIAGLFLGGVGMGVGTAVTVMFQWRVSFAFIENNIIVVFENFWEGLMNCVROANI 60
PR	29-SEP-1998;	98US-0102207P.	XX			XX	Db 1 MATHALEIAGLFLGGVGMGVGTAVTVMFQWRVSFAFIENNIIVVFENFWEGLMNCVROANI 60
PR	29-SEP-1998;	98US-0102240P.	XX			XX	QY 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
PR	29-SEP-1998;	98US-0102307P.	XX			XX	Db 61 RMQCKIYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDNKVKAHILL 120
PR	29-SEP-1998;	98US-0102330P.	XX			XX	QY 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSIVNVAQKRELGEALYLGTWTLVIVGGA 180
PR	30-SEP-1998;	98US-0102484P.	XX			XX	Db 121 TAGIIFIITGMVLLIPVSWANAIIRDYFNSIVNVAQKRELGEALYLGTWTLVIVGGA 180
PR	30-SEP-1998;	98US-0102487P.	XX			XX	QY 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
PR	30-SEP-1998;	98US-0102570P.	XX			XX	Db 181 LFCVFCCKNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYSRSQYV 225
PR	30-SEP-1998;	98US-0102571P.	XX			XX	QY
PR	01-OCT-1998;	98US-0102684P.	XX			XX	Db
PR	01-OCT-1998;	98US-0102687P.	XX			XX	QY
PR	02-OCT-1998;	98US-0102965P.	XX			XX	Db
PR	06-OCT-1998;	98US-0103258P.	XX			XX	QY
PR	06-OCT-1998;	98US-0103449P.	XX			XX	Db
PR	07-OCT-1998;	98US-0103314P.	XX			XX	QY
PR	07-OCT-1998;	98US-0103315P.	XX			XX	Db
PR	07-OCT-1998;	98US-0103328P.	XX			XX	QY
PR	07-OCT-1998;	98US-0103395P.	XX			XX	Db
PR	07-OCT-1998;	98US-0103396P.	XX			XX	QY
PR	07-OCT-1998;	98US-0103401P.	XX			XX	Db
PR	08-OCT-1998;	98US-0103633P.	XX			XX	QY
PR	08-OCT-1998;	98US-0103678P.	XX			XX	Db
PR	08-OCT-1998;	98US-0103679P.	XX			XX	QY
PR	08-OCT-1998;	98US-0103711P.	XX			XX	Db
PR	14-OCT-1998;	98US-0104257P.	XX			XX	QY
PR	20-OCT-1998;	98US-0104987P.	XX			XX	Db
PR	20-OCT-1998;	98US-0105000P.	XX			XX	QY
PR	20-OCT-1998;	98US-0105002P.	XX			XX	Db
PR	21-OCT-1998;	98US-0105104P.	XX			XX	QY
PR	22-OCT-1998;	98US-0105169P.	XX			XX	Db
PR	22-OCT-1998;	98US-0105266P.	XX			XX	QY
PR	26-OCT-1998;	98US-0105693P.	XX			XX	Db
PR	26-OCT-1998;	98US-0105694P.	XX			XX	QY
PR	27-OCT-1998;	98US-0105807P.	XX			XX	Db
PR	27-OCT-1998;	98US-0105881P.	XX			XX	QY
PR	27-OCT-1998;	98US-0105882P.	XX			XX	Db
PR	27-OCT-1998;	98US-0106023P.	XX			XX	QY
PR	28-OCT-1998;	98US-0106023P.	XX			XX	Db
PR	28-OCT-1998;	98US-0106030P.	XX			XX	QY
PR	28-OCT-1998;	98US-0106032P.	XX			XX	Db
PR	28-OCT-1998;	98US-0106033P.	XX			XX	QY
PR	28-OCT-1998;	98US-0106178P.	XX			XX	Db
PR	29-OCT-1998;	98US-0106248P.	XX			XX	QY
PR	29-OCT-1998;	98US-0106384P.	XX			XX	Db
PR	29-OCT-1998;	98US-0108500P.	XX			XX	QY
PR	30-OCT-1998;	98US-0108464P.	XX			XX	Db
PR	03-NOV-1998;	98US-0106856P.	XX			XX	QY
PR	03-NOV-1998;	98US-0106902P.	XX			XX	Db

RESULT 2
AAB66182
ID AAB66182 standard; protein; 225 AA.
XX

```

AACB66182;
XX
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #94.
XX
XX Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX
XX 20-JUL-1999; 99US-0144758P.
XX
XX 26-JUL-1999; 99US-0145698P.
XX
XX 01-SEP-1999; 99WO-US020111.
XX
XX 29-OCT-1999; 99US-0162506P.
XX
XX 30-NOV-1999; 99WO-US028313.
XX
XX 02-DEC-1999; 99WO-US028551.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 05-JAN-2000; 2000WO-US000219.
XX
XX 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 1; Fig 188; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy
XX
XX Sequence 225 AA;
XX
XX Query Match 100.0%; Score 225; DB 4; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-212;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MATHALEIAGLFLGGVGMGTVAVTWMPQWVSFAFIENNIIVVFENFWEGLMNCVQANI 60
XX Db 1 MATHALEIAGLFLGGVGMGTVAVTWMPQWVSFAFIENNIIVVFENFWEGLMNCVQANI 60
XX
XX QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
XX Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
XX
XX QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSVNVVNAOKRELGEALYLGWTTALVLIYVGA 180
XX Db 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSVNVVNAOKRELGEALYLGWTTALVLIYVGA 180
XX
XX QY 181 LFCVFCCKSSSYRYSIPSHRTQKSYHTGKSPSVYRSQVY 225
XX Db 181 LFCVFCCKSSSYRYSIPSHRTQKSYHTGKSPSVYRSQVY 225

```

```

RESULT 3
AAM78572
ID AAM78572 standard; protein; 225 AA.
XX
XX AAM78572;
AC
XX 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 1234.
XX
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK51705.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 3493-3494; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
XX
XX Sequence 225 AA;
XX
XX Query Match 100.0%; Score 225; DB 4; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-212;
XX Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MATHALEIAGLFLGGVGMGTVAVTWMPQWVSFAFIENNIIVVFENFWEGLMNCVQANI 60
XX Db 1 MATHALEIAGLFLGGVGMGTVAVTWMPQWVSFAFIENNIIVVFENFWEGLMNCVQANI 60
XX
XX QY 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120
XX Db 61 RMOCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTCTGDNKVKAHILL 120

```

PA (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-602746/68.
XX N-PSDB; AAS46103.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 358; 774pp; English.
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 225 AA;
XX
Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGMVGTVAIVMPQWRVSAFTENNIVFENFEGLMNVCVRQANI 60
DB 1 MATHALEIAGLFLGGVGMVGTVAIVMPQWRVSAFTENNIVFENFEGLMNVCVRQANI 60
QY 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTCTGDNKVKAHILL 120
DB 61 RMCKIYDSLALSPDLQAARGLMCAASVMSFLAFMAILGKCTCTGDNKVKAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
DB 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCNCKSSRYRISPSHRTTQKSYHTGKSPSVYRSQYV 225
DB 181 LFCVFCNCKSSRYRISPSHRTTQKSYHTGKSPSVYRSQYV 225
RESULT 5
AAB87585
ID AAB87585 standard; protein; 225 AA.
XX
XX AAB87585;
XX
XX 15-MAY-2001 (first entry)
DT
XX
XX Human PRO1573.
DE
XX
XX Human; PRO protein; mapping.
KW
XX
XX Homo sapiens.
OS
XX WO200116318-A2.
PN
XX
XX 08-MAR-2001.
PD
XX
XX 24-AUG-2000; 2000WO-US023328.
PF

QY 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
DB 121 TAGIIFIITGMVLLIPVSWANAIIRDYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
QY 181 LFCVFCNCKSSRYRISPSHRTTQKSYHTGKSPSVYRSQYV 225
DB 181 LFCVFCNCKSSRYRISPSHRTTQKSYHTGKSPSVYRSQYV 225
RESULT 4
AAU29202
ID AAU29202 standard; protein; 225 AA.
XX
XX AAU29202;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human PRO polypeptide sequence #179.
DE
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200168848-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 28-FEB-2001; 2001WO-US006520.
PF
XX
XX 01-MAR-2000; 2000WO-US005601.
PR
XX 02-MAR-2000; 2000WO-US005841.
PR
XX 03-MAR-2000; 2000US-0187202P.
PR
XX 06-MAR-2000; 2000US-0186968P.
PR
XX 14-MAR-2000; 2000US-0189320P.
PR
XX 14-MAR-2000; 2000US-0189328P.
PR
XX 15-MAR-2000; 2000WO-US006884.
PR
XX 21-MAR-2000; 2000US-0190828P.
PR
XX 21-MAR-2000; 2000US-0191007P.
PR
XX 21-MAR-2000; 2000US-0191048P.
PR
XX 21-MAR-2000; 2000US-0191314P.
PR
XX 28-MAR-2000; 2000US-0192655P.
PR
XX 29-MAR-2000; 2000US-0193032P.
PR
XX 29-MAR-2000; 2000US-0193053P.
PR
XX 30-MAR-2000; 2000WO-US008439.
PR
XX 04-APR-2000; 2000US-0194449P.
PR
XX 04-APR-2000; 2000US-0194647P.
PR
XX 11-APR-2000; 2000US-0195975P.
PR
XX 11-APR-2000; 2000US-0196000P.
PR
XX 11-APR-2000; 2000US-0196187P.
PR
XX 11-APR-2000; 2000US-0196690P.
PR
XX 11-APR-2000; 2000US-0196820P.
PR
XX 18-APR-2000; 2000US-0198121P.
PR
XX 18-APR-2000; 2000US-0198585P.
PR
XX 25-APR-2000; 2000US-0199397P.
PR
XX 25-APR-2000; 2000US-0199550P.
PR
XX 25-APR-2000; 2000US-0199654P.
PR
XX 03-MAY-2000; 2000US-0201516P.
PR
XX 17-MAY-2000; 2000WO-US013705.
PR
XX 22-MAY-2000; 2000WO-US014042.
PR
XX 30-MAY-2000; 2000WO-US014941.
PR
XX 02-JUN-2000; 2000WO-US015284.
PR
XX 05-JUN-2000; 2000US-0203832P.
PR
XX 28-JUL-2000; 2000WO-US020710.
PR
XX 22-AUG-2000; 2000US-00644848.
PR
XX 24-AUG-2000; 2000WO-US023328.
PR
XX 08-NOV-2000; 2000WO-US030952.
PR
XX 01-DEC-2000; 2000WO-US032678.
PR
XX 20-DEC-2000; 2000WO-US034956.
XX

XX PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CU, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-183260/18.
 DR N-PSDB; AAP92117.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 12; Fig 120; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping
 XX
 SQ Sequence 225 AA;
 Query Match 100.0%; Score 225; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNIIVVFENFWEGLMNCVQANI 60
 DB 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNIIVVFENFWEGLMNCVQANI 60
 QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNKVKAHILL 120
 DB 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 QY 181 LFCVFCCKEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQV 225
 DB 181 LFCVFCCKEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQV 225
 RESULT 6
 AAG89285
 ID AAG89285 standard; protein; 225 AA.
 XX
 AC AAG89285;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 405.
 XX

KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
 KW GENSET.
 XX
 OS Homo sapiens.
 XX
 PN WO200142451-A2.
 XX
 PD 14-JUN-2001.
 XX
 XX 07-DEC-2000; 2000WO-IB001938.
 XX
 XX 08-DEC-1999; 99US-0169629P.
 PR 06-MAR-2000; 2000US-0187470P.
 XX
 XX (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
 XX
 DR WPI; 2001-367870/38.
 DR N-PSDB; AAH64888.
 XX
 PT Full length GENSET human nucleic acids encoding potentially secreted
 PT proteins, useful in gene therapy and vaccination against a variety of
 PT diseases, and for diagnosis of those diseases.
 XX
 PS Claim 21; Page 885-886; 921pp; English.
 XX
 CC The invention relates to full length GENSET human nucleic acids encoding
 CC potentially secreted proteins. The nucleic acids and the polypeptides
 CC they encode may be used in the prevention, treatment and diagnosis of
 CC diseases associated with inappropriate GENSET gene expression. For
 CC example, they be used to treat disorders associated with decreased GENSET
 CC gene expression by rectifying mutations or deletions in a patient's
 CC genome that affect the activity of GENSET or by supplementing the
 CC patients own production of GENSET polypeptides. Conversely, antisense
 CC nucleic acid molecules may be administered to down regulate GENSET
 CC expression by binding with the cells' own genes and preventing their
 CC expression. The sense and antisense nucleic acids may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and hence to determine which
 CC patients may be in need of restorative therapy. The GENSET polypeptides
 CC may be used as antigens in the production of antibodies and in assays to
 CC identify modulators (agonists and antagonists) of GENSET polypeptide
 CC expression and activity. The present sequence is a GENSET polypeptide of
 CC the invention
 XX
 SQ Sequence 225 AA;
 Query Match 100.0%; Score 225; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNIIVVFENFWEGLMNCVQANI 60
 DB 1 MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSFAFIENNIIVVFENFWEGLMNCVQANI 60
 QY 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNKVKAHILL 120
 DB 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKTRCTGDNKVKAHILL 120
 QY 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 DB 121 TAGIIFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
 QY 181 LFCVFCCKEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQV 225
 DB 181 LFCVFCCKEKSSSYRYSIPSHRTTQKSYHTGKKSPPSVYSRSQV 225
 RESULT 7
 ABG95910
 ID ABG95910 standard; protein; 225 AA.
 XX

AC ABG9591.0;
 XX 10-DEC-2002 (first entry)
 DT
 XX Human secreted/transmembrane protein PRO1573.
 DE
 XX Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX US2002119130-A1.
 XX 29-AUG-2002.
 XX 06-DEC-2001; 2001US-00006867.
 XX 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 29-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-00889105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089653P.
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 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 26-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
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 PR 17-AUG-1998; 98US-0096757P.
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 PR 23-SEP-1998; 98US-0101475P.
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 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103443P.
 PR 08-MAR-1999; 98US-0103498P.
 PR 14-MAY-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US010733.
 PR 01-SEP-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2002-731348/79.
 N-PSDB; ABS74437.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 120; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19780 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome

CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 225; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATHALEIAGLFLGGVGVGTAVTVPQWRYSARIENNIVVFENFWGLWNCVRQANI 60
Db 1 MATHALEIAGLFLGGVGVGTAVTVPQWRYSARIENNIVVFENFWGLWNCVRQANI 60
QY 61 RMQCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVAHILL 120
Db 61 RMQCKIYDLSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVAHILL 120
QY 121 TAGIIFIITGMVLLIPVSWVANAIIRDVNSIVNVAQRELGEALYLGWTTALVIVGGA 180
Db 121 TAGIIFIITGMVLLIPVSWVANAIIRDVNSIVNVAQRELGEALYLGWTTALVIVGGA 180
QY 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSVHTGKSPSVYSRQYV 225
Db 181 LFCCVFCCKNEKSSSYRYSIPSHRTTQKSVHTGKSPSVYSRQYV 225

RESULT 8

ABU58578
ID ABU58578 standard; protein; 225 AA.
XX
AC ABU58578;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #179.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
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PR 22-JUN-1998; 98US-0090246P.
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PR 24-JUN-1998; 98US-0090429P.

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PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090678P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090690P.	PR	02-OCT-1998;	98US-0102965P.
PR	25-JUN-1998;	98US-0090694P.	PR	06-OCT-1998;	98US-0103258P.
PR	25-JUN-1998;	98US-0090695P.	PR	06-OCT-1998;	98US-0103449P.
PR	25-JUN-1998;	98US-0090696P.	PR	07-OCT-1998;	98US-00168978.
PR	26-JUN-1998;	98US-00105413.	Query Match 100.0%; Score 225; DB 6; Length 225;		
PR	26-JUN-1998;	98US-0090862P.	Best Local Similarity 100.0%; Pred. No. 3.2e-212; Indels 0; Gaps 0;		
PR	26-JUN-1998;	98US-0090863P.	Matches 225; Conservative 0; Mismatches 0;		
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PR	01-JUL-1998;	98US-0091359P.	QY	1	MATHALETAGFLGGVGMGTVAVTVMPOWRYSAFIENNVVVFENFWEGLMNCVRQANI 60
PR	01-JUL-1998;	98US-0091544P.	Db	1	MATHALETAGFLGGVGMGTVAVTVMPOWRYSAFIENNVVVFENFWEGLMNCVRQANI 60
PR	02-JUL-1998;	98US-0091478P.	QY	61	RMQCKIYDSLALSEDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGNEKVKAHILL 120
PR	02-JUL-1998;	98US-0091486P.	Db	61	RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTRCTGNEKVKAHILL 120
PR	02-JUL-1998;	98US-0091626P.	QY	121	TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
PR	02-JUL-1998;	98US-0091628P.	Db	121	TAGIIFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGA 180
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PR	10-AUG-1998;	98US-0095988P.	Db	181	LFCCVFCCKNEKSSSRYRISPSHRTTQKSYHTGKKSFSVYSRSQYV 225
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PR	17-AUG-1998;	98US-0096867P.	XX	AC	ABU88126;
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PR	17-AUG-1998;	98US-0096897P.	XX	Novel human secreted and transmembrane protein	PRO1573.
PR	18-AUG-1998;	98US-0096949P.	XX	Human; secreted and transmembrane protein: PRO; gene therapy;	
PR	18-AUG-1998;	98US-0096959P.	KW	tumour necrosis factor-alpha release; TNF-alpha release;	
PR	18-AUG-1998;	98US-0097022P.	KW	chondrocyte proliferation; chondrocyte differentiation; tumour;	
PR	26-AUG-1998;	98US-0097952P.	KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	
PR	26-AUG-1998;	98US-0097954P.	KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
PR	26-AUG-1998;	98US-0097955P.	XX	Homo sapiens.	
PR	26-AUG-1998;	98US-0097971P.	OS	US2003032127-A1.	
PR	26-AUG-1998;	98US-0097974P.	PN	13-FEB-2003.	
PR	26-AUG-1998;	98US-0098011P.	PD	26-JUN-2002;	2002US-00183012.
PR	01-SEP-1998;	98US-0098716P.	PF	18-SEP-1997;	97US-0059263P.
PR	01-SEP-1998;	98US-0098723P.	XX	18-SEP-1997;	97US-0059266P.
PR	02-SEP-1998;	98US-0098803P.	PR	17-OCT-1997;	97US-0062250P.
PR	02-SEP-1998;	98US-0098821P.	PR	21-OCT-1997;	97US-0063486P.
PR	02-SEP-1998;	98US-0098843P.	PR	24-OCT-1997;	97US-0063120P.
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PR	16-SEP-1998;	98US-0100662P.	PR	31-OCT-1997;	97US-0063870P.
PR	16-SEP-1998;	98US-0101751P.	PR	31-OCT-1997;	97US-0064103P.
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PR	29-SEP-1998;	98US-0102207P.			

PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069333P.
PR 12-DEC-1997; 97US-0069425P.
PR 18-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
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PR 27-MAR-1998; 98US-0079664P.
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PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 08-APR-1998; 98US-0080333P.
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PR 09-APR-1998; 98US-0081195P.
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Qy 61 RMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGKCTCTGDKNEKVAHILL 120
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Qy 121 TAGIIFIITGMVLIPIVSWANAIIRDYFNSIVNVAQKRELGEALYLGWTTALVIVGGA 180
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DT 05-AUG-2003 (first entry)
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extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy.
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OS Homo sapiens.
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PN US2003027278-A1.
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PD 06-FEB-2003.
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PF 21-JUN-2002; 2002US-00176987.
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XX		PR 04-JUN-1998;	98US-0088029P.
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XX	US2003036147-Al.	PR 04-JUN-1998;	98US-0088326P.
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QY 121 TAGIFITIGMVLIPVSWANAIIRFYSINVNAOKRELGEALYLGWTTALVIVGGA 180
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QY 181 LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225
Db 181 LFCCVFCNEKSSSYRYSIPSHRTTQKSYHTGKSPSVYRSQYV 225

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